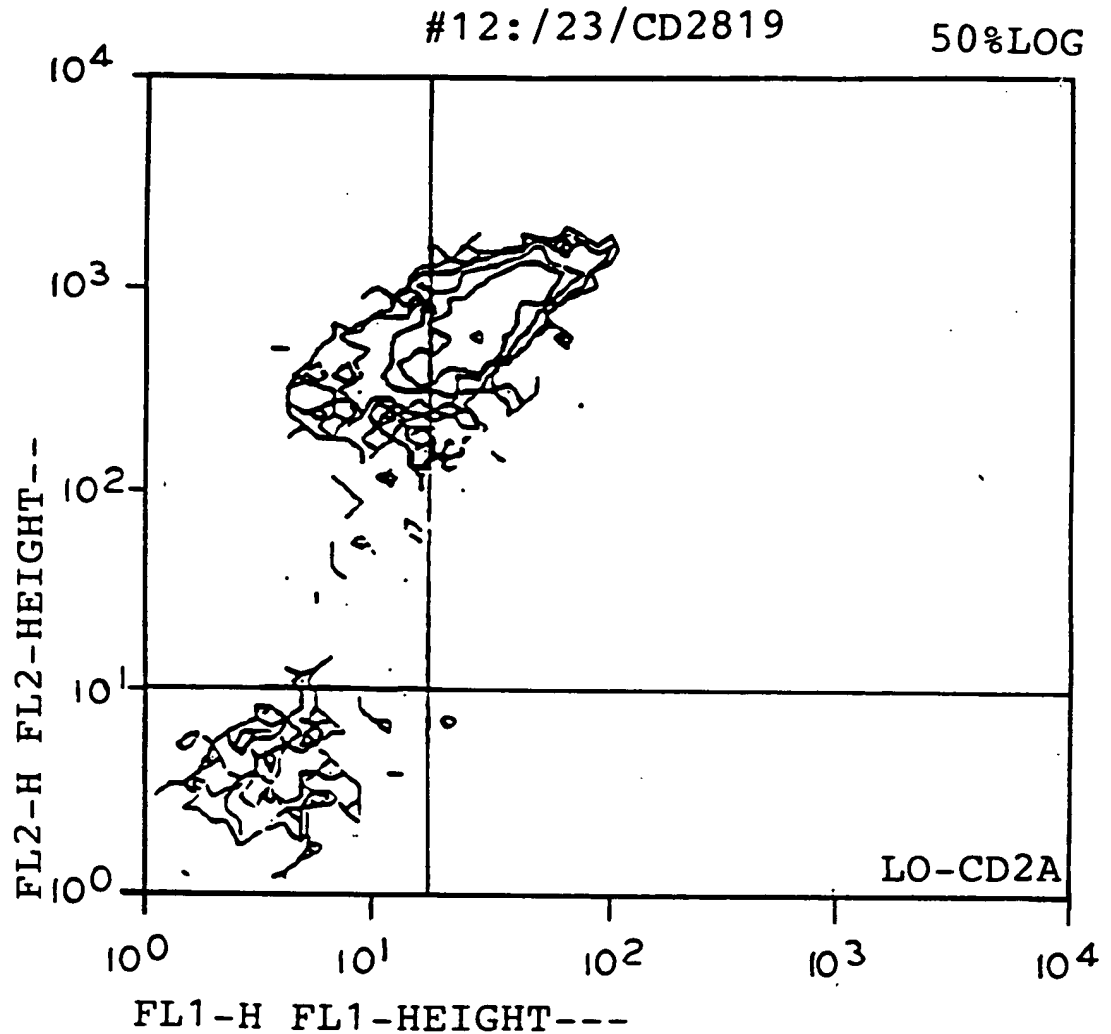


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FIG. 1



#12:/23/CD2019

---QUAD STATS---

FILE: #12:/23/CD2019 SAMPLE: 059

DATE: 9/24/92 GATE G1-R1

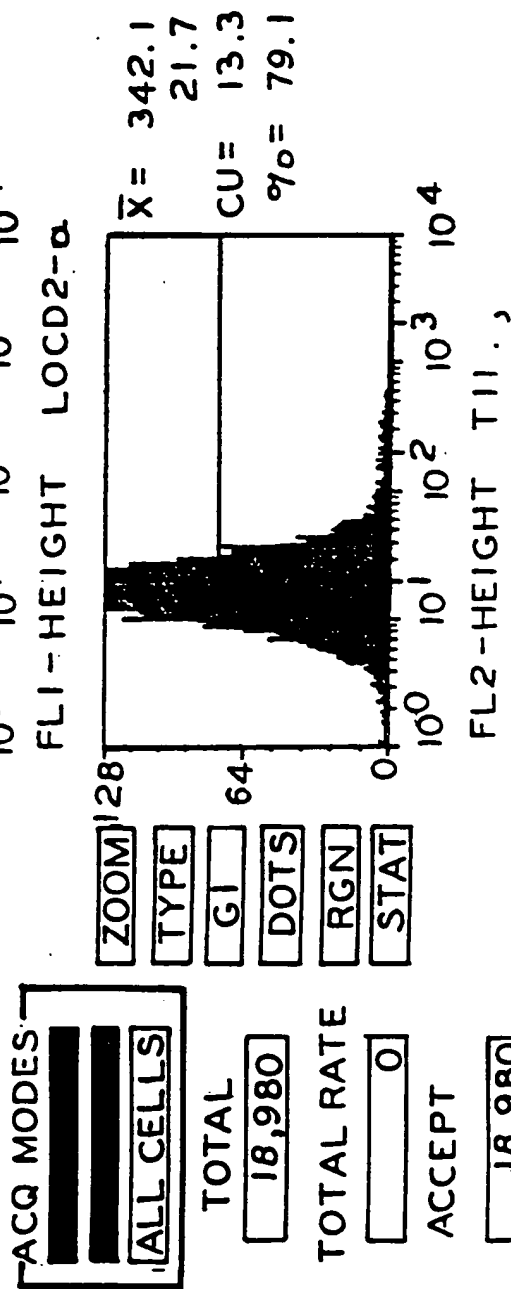
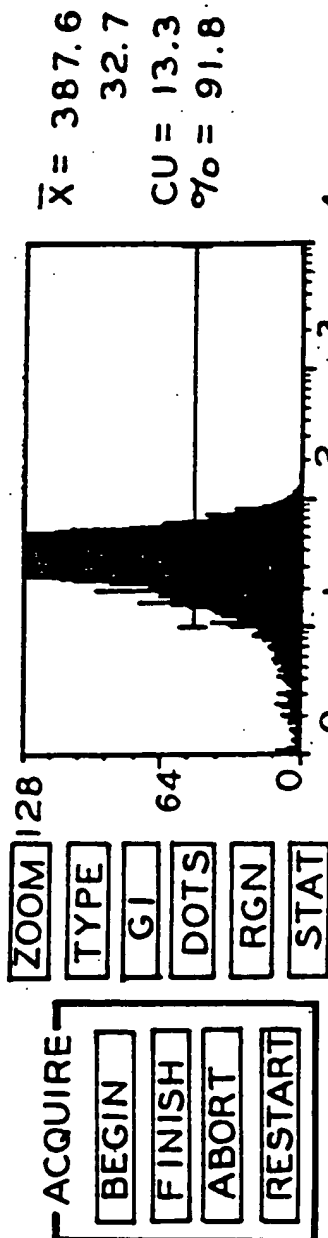
PARMETER: FL1-H (LOG) FL2-H(LOG) QUAD

LOCATION:17.15.9

TOTAL=	5000	GATED=	L290		
QUAD	EVENTS	% GATED	%TOTAL	X MEAN	Y MEAN
----	-----	-----	-----	-----	-----
IUL	299	23.18	3.98	11.41	284.69
2UR	851	65.97	17.02	32.70	630.65
3LL	135	10.47	2.70	4.08	3.31
4LR	5	0.39	0.10	25.11	6.54

862040" 22095060

ACO CMD INST-CTRL GATES FORMAT PROTO SAVE



TOTAL

18,980

TOTAL RATE

0

ACCEPT

18,980

ELAPSED TIME

00:00:48

FIG. 2A

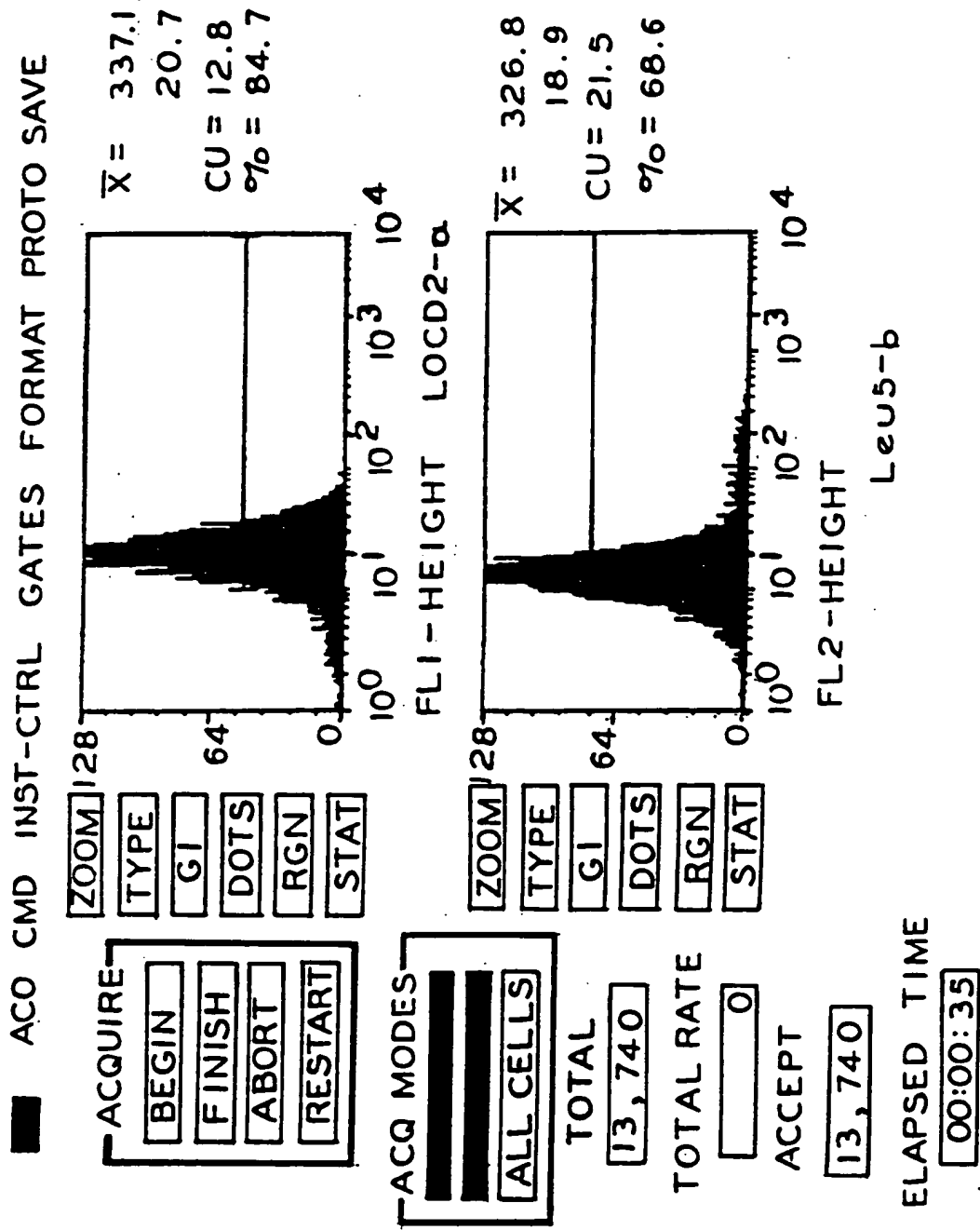


FIG. 2B

FIG. 3A

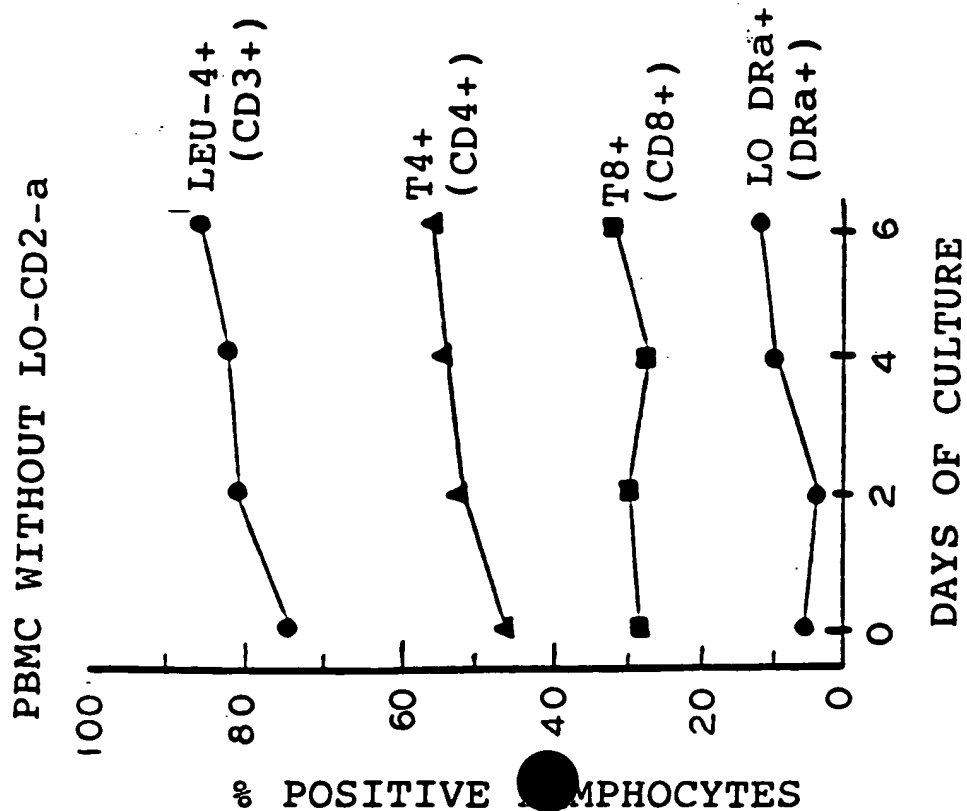


FIG. 3B

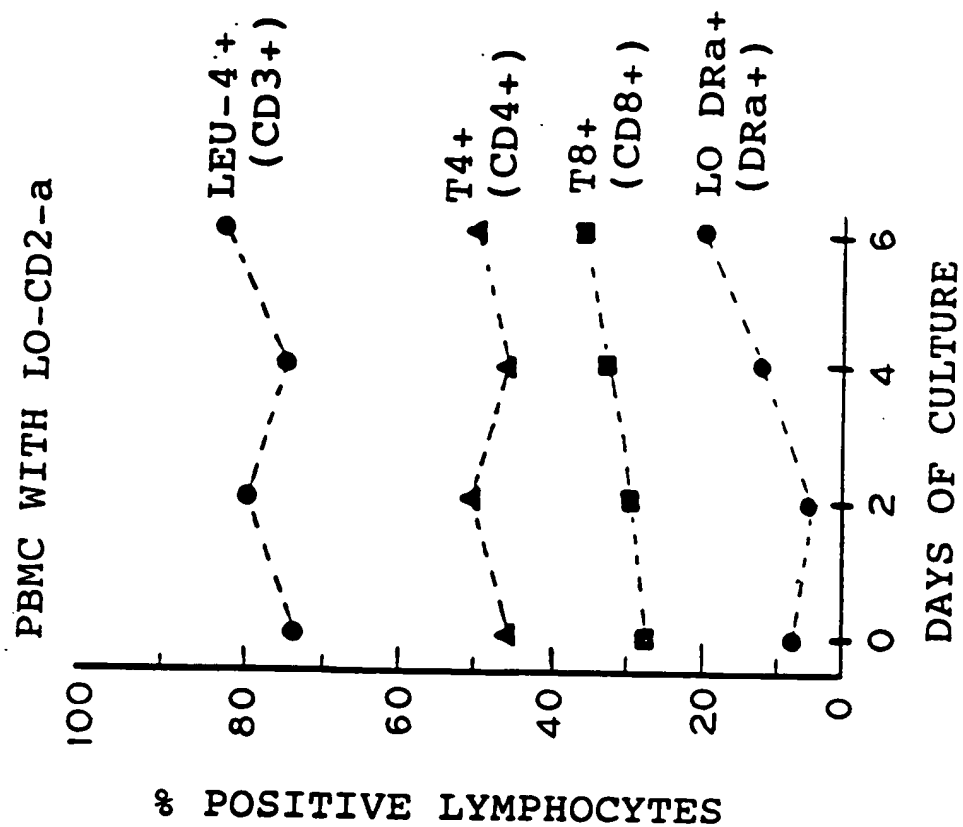
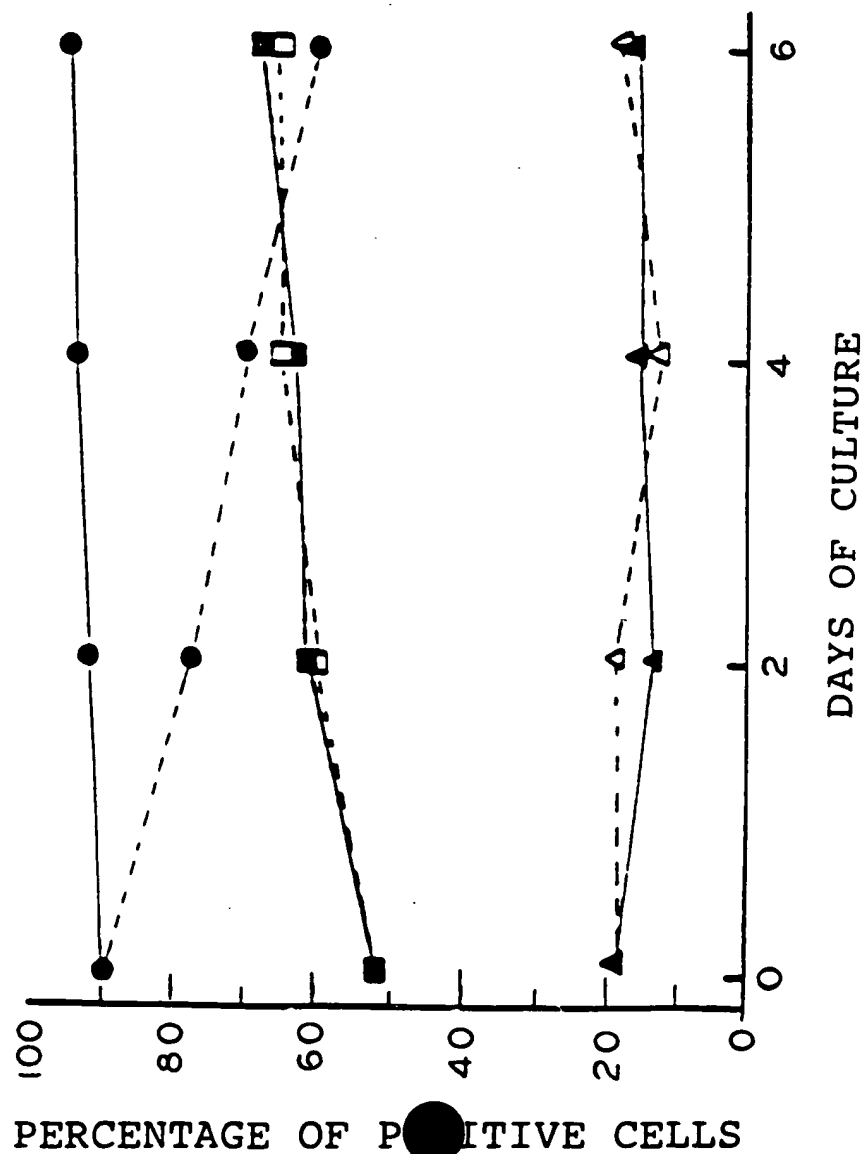


FIG. 4

PBMC: PHENOTYPICAL ANALYSIS



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FIG. 5A

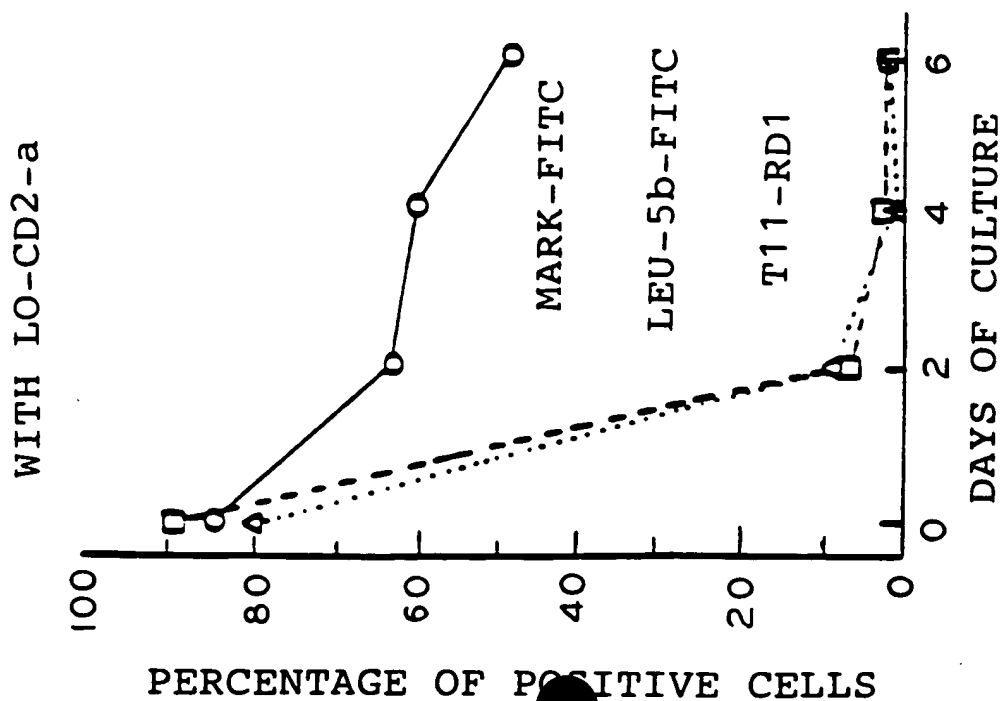
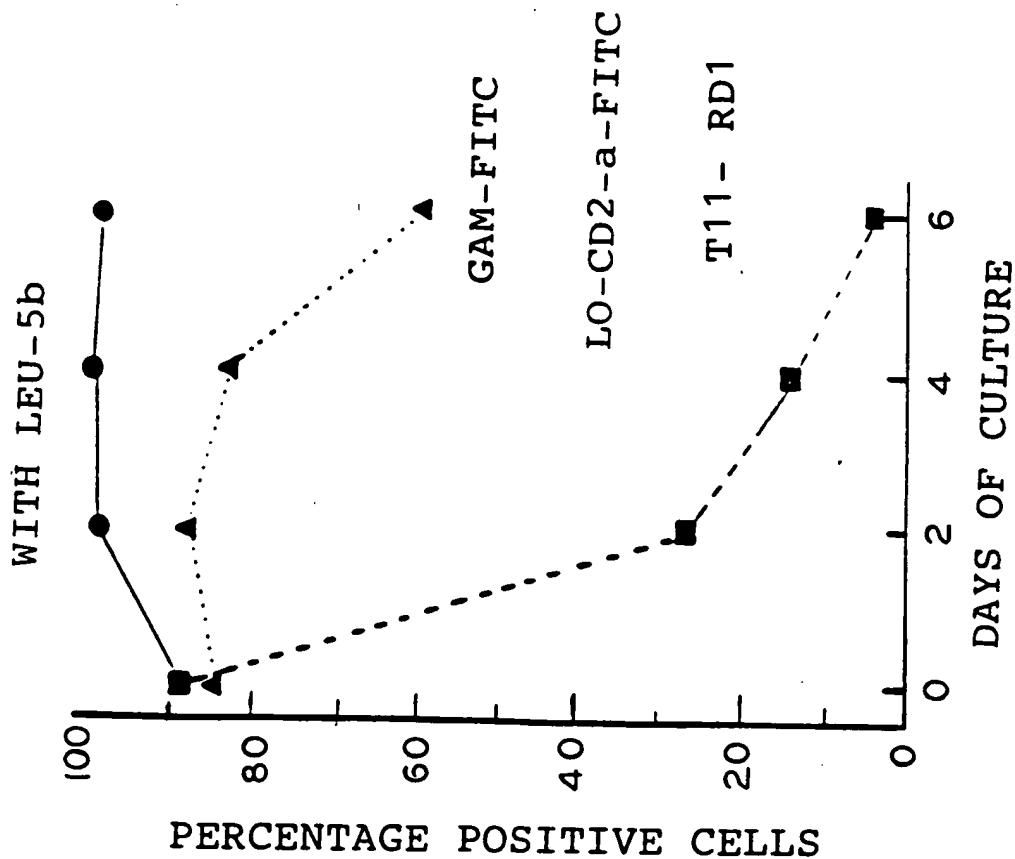


FIG. 5B



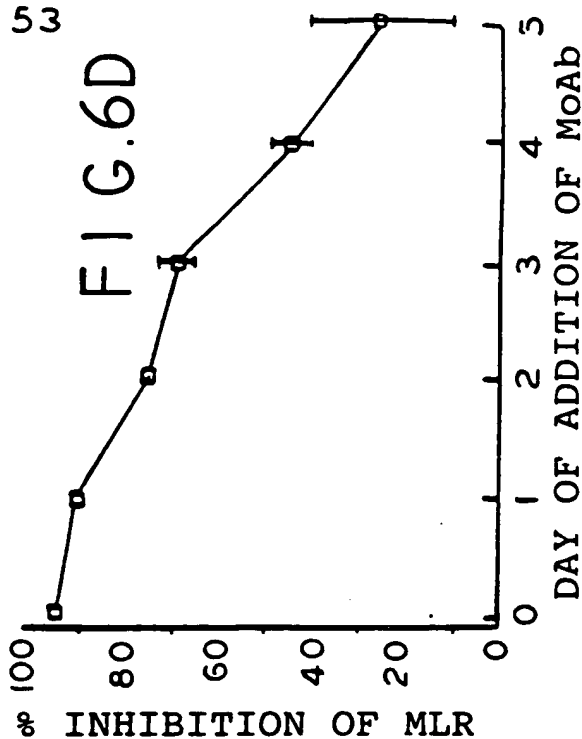
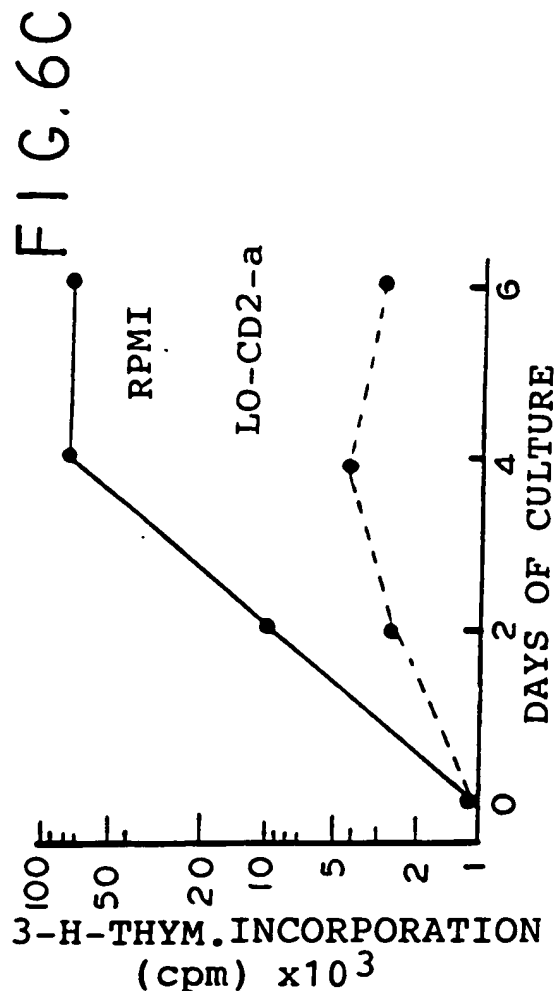
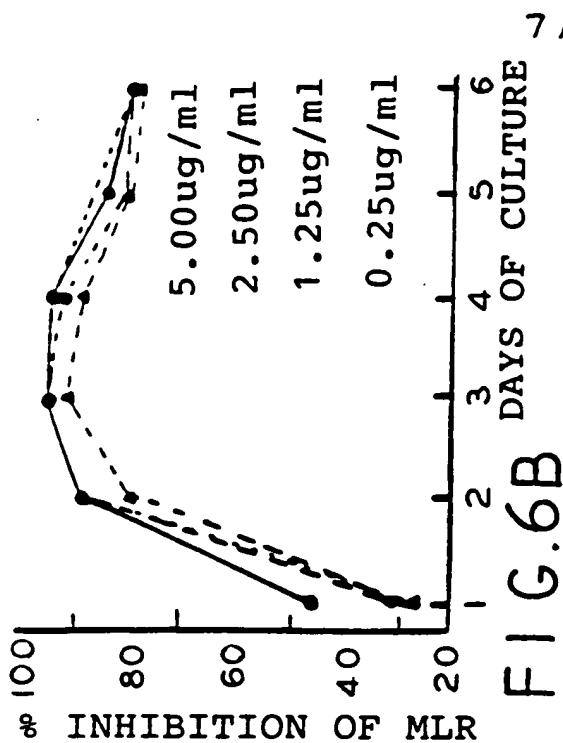
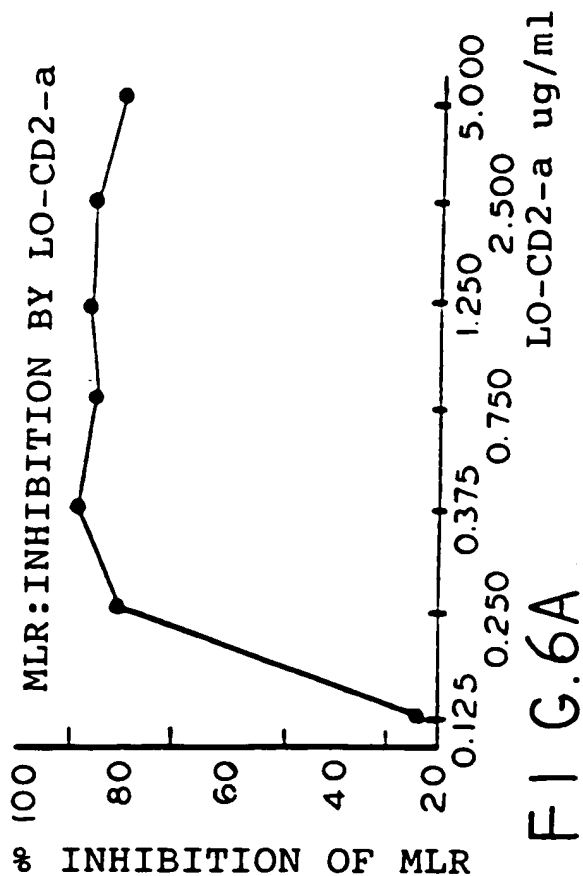


FIG. 7A

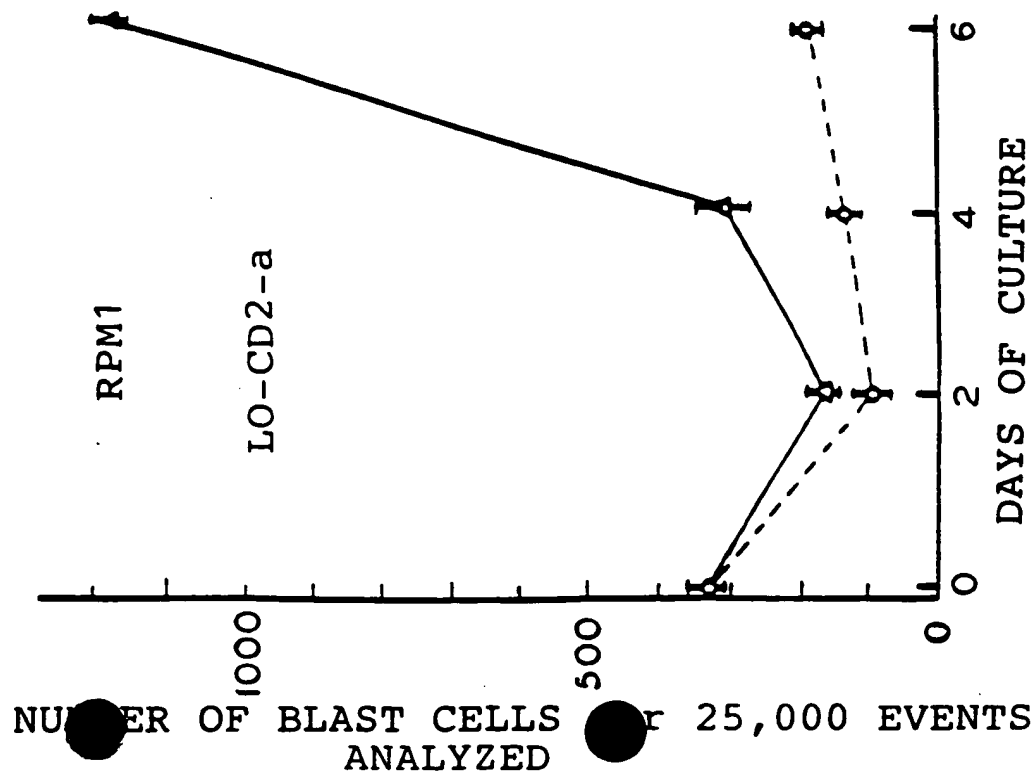
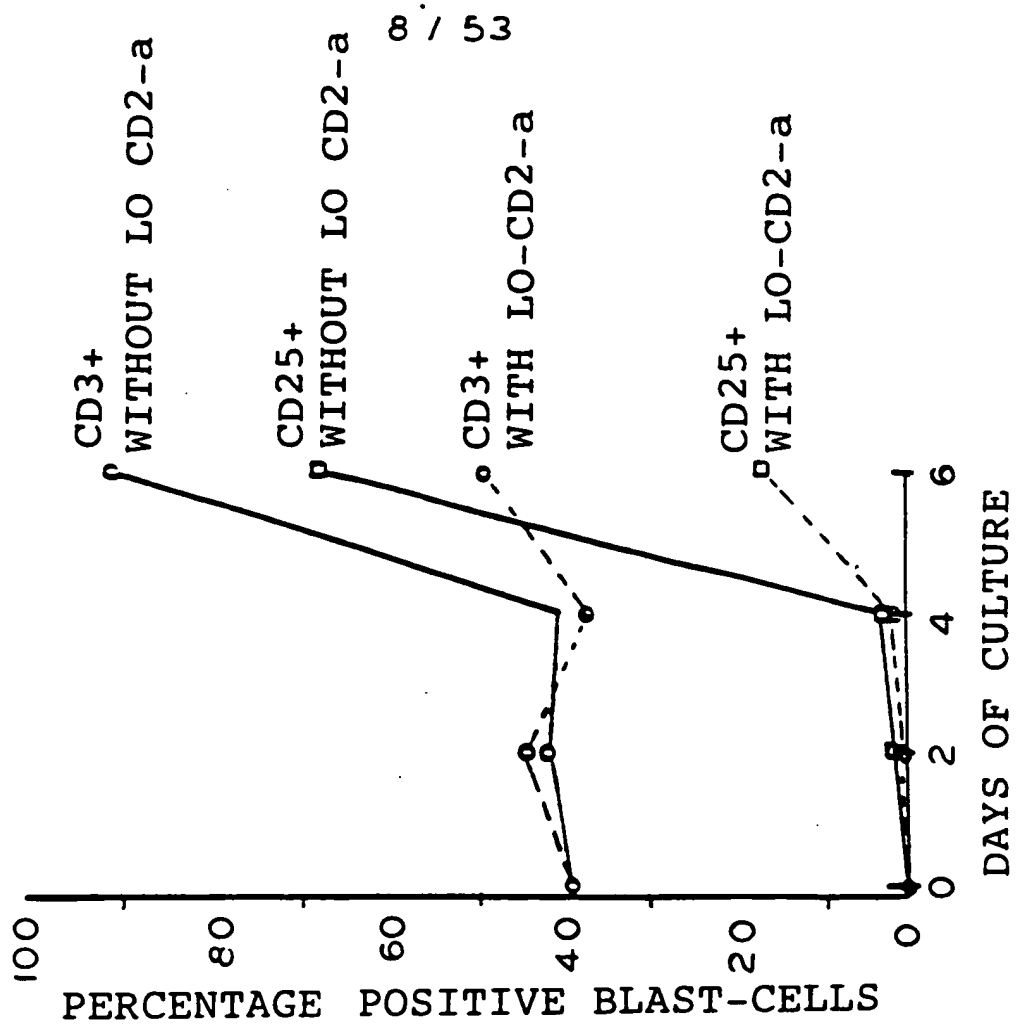
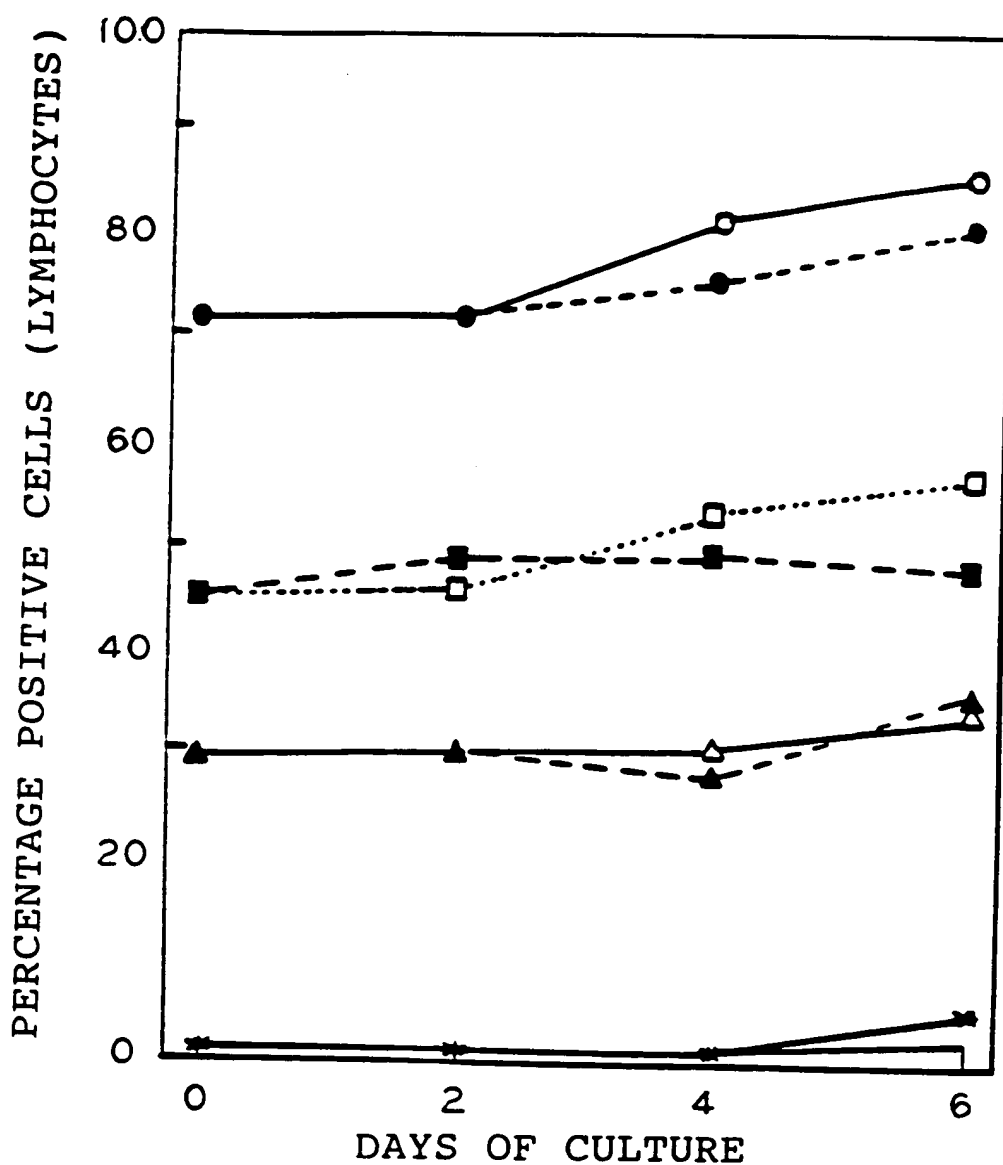


FIG. 7B



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FIG. 8A



CD3+ (-MoAb) CD3+ (-MoAb)

CD8+ (-MoAb) CD8+ (+MoAb)

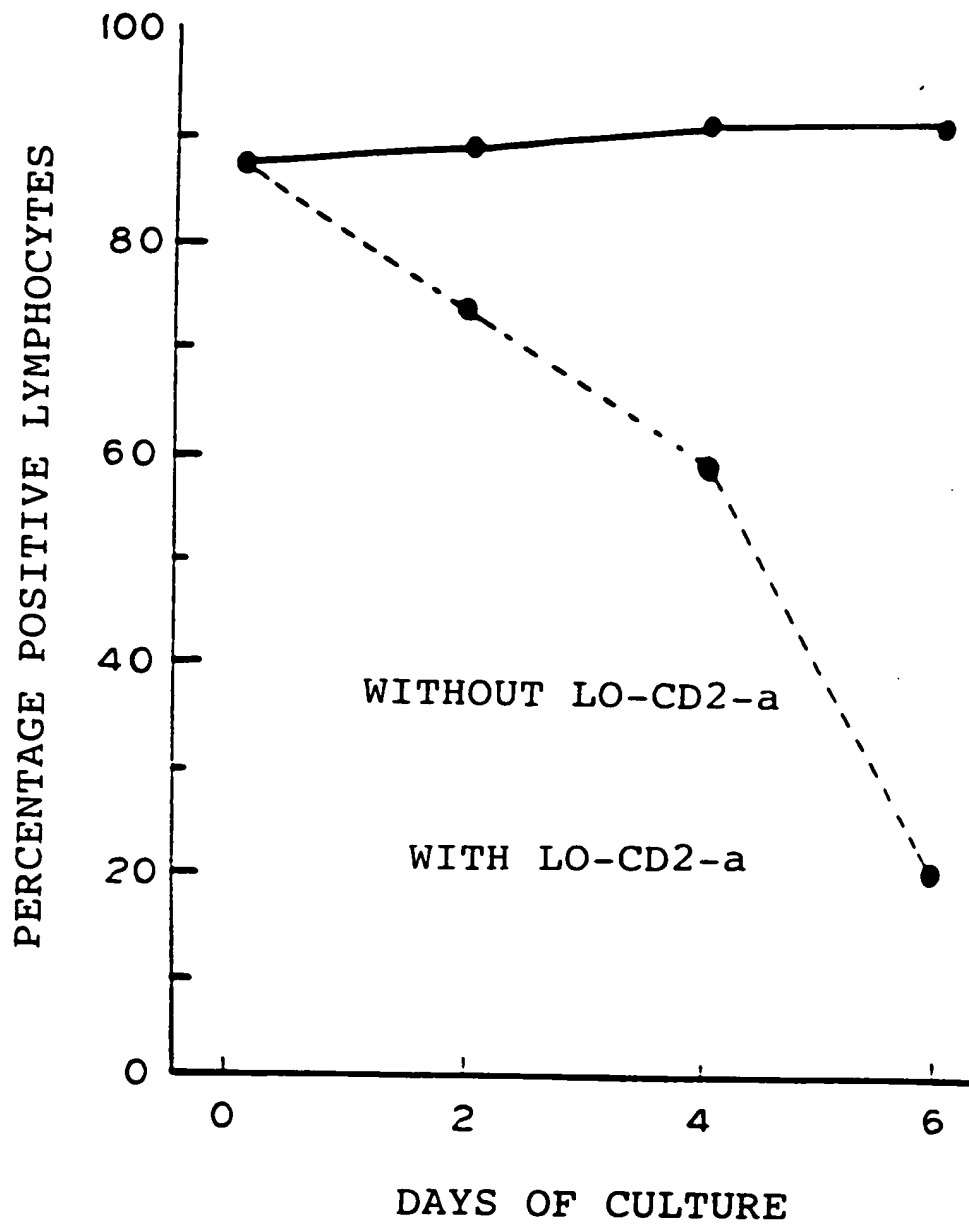
CD4+ (-MoAb) CD4+ (-MoAb)

CD25+ (-MoAb) CD25+ (+MoAb)

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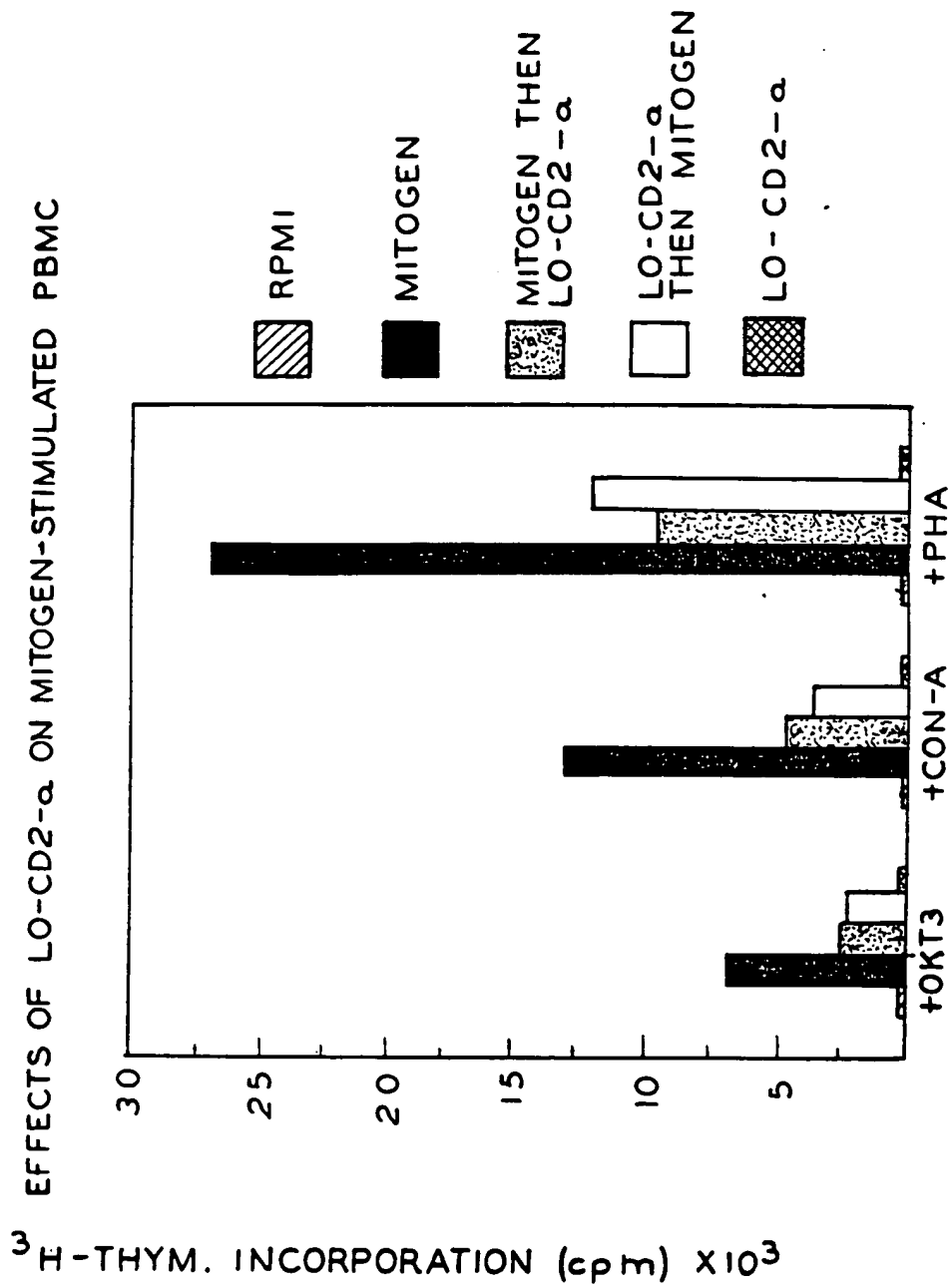
FIG. 8B

MLC:LEU-56+(CD2+) CELLS



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FIG. 9



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FIG. 10

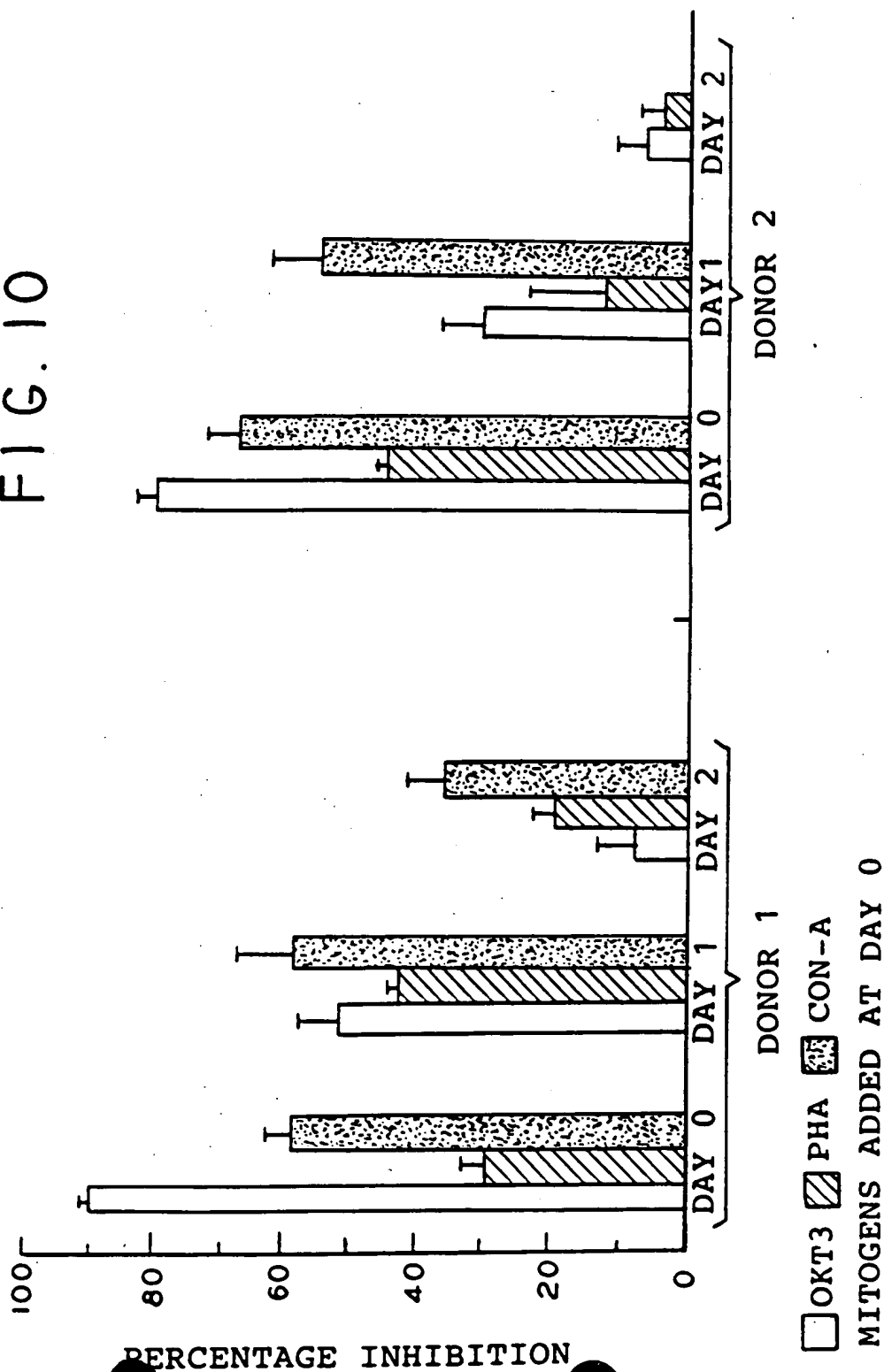
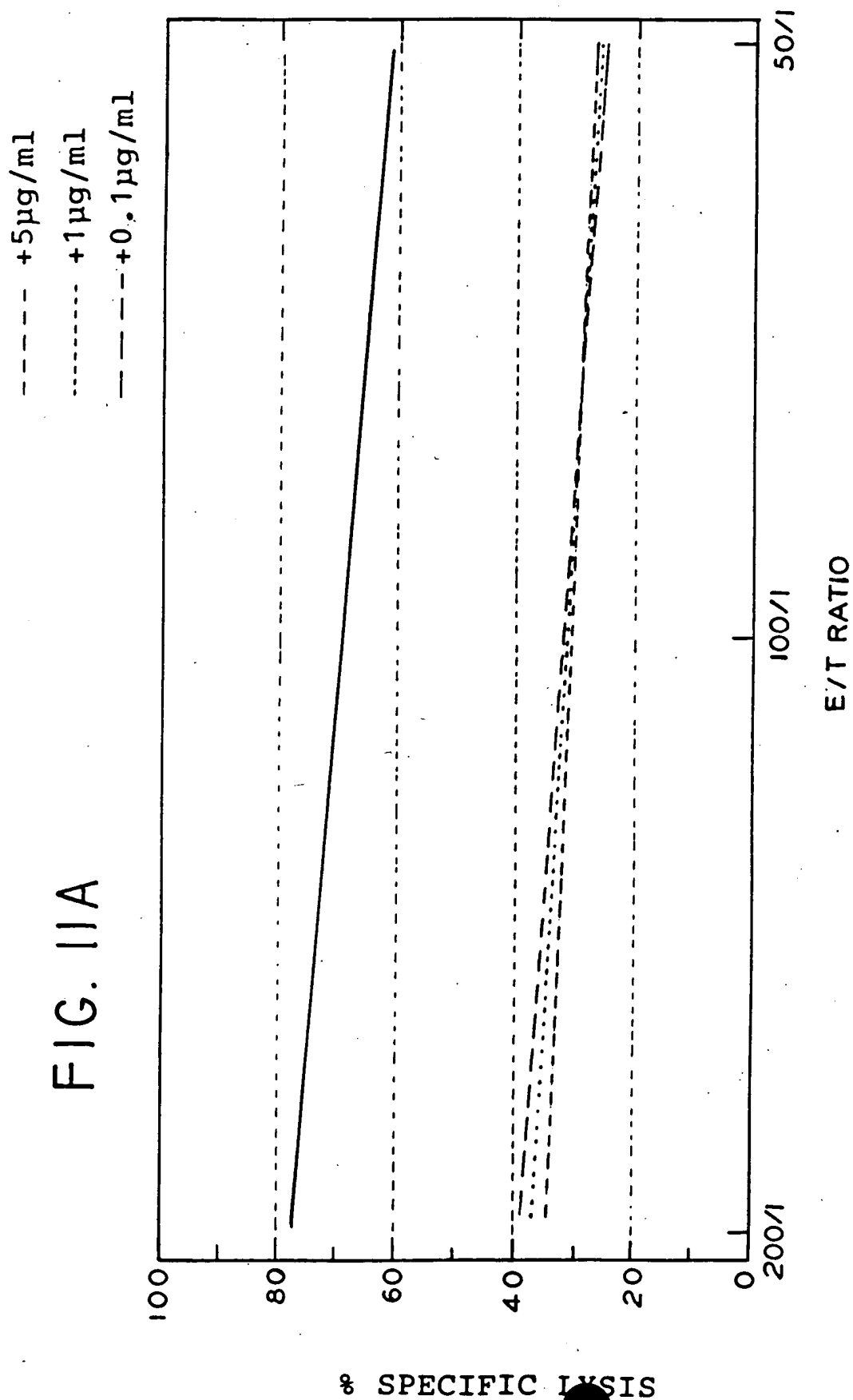


FIG. IIA

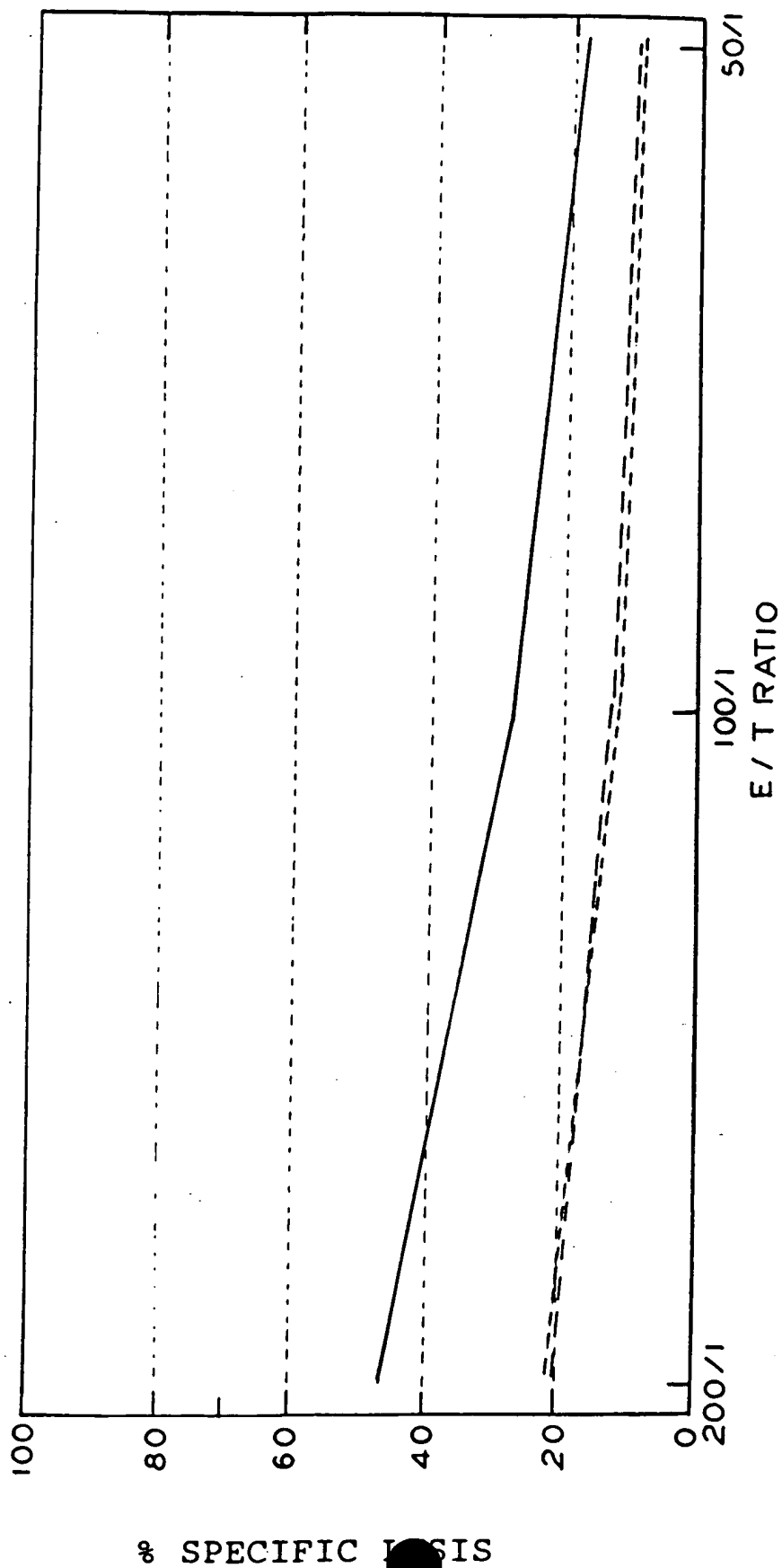


% SPECIFIC LYSIS

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----- + 5 μ g/ml
 - - - - - + 1 μ g/ml
 ----- + 0.1 μ g/ml

FIG. IIB



% SPECIFIC INHIBITION

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FIG. 12

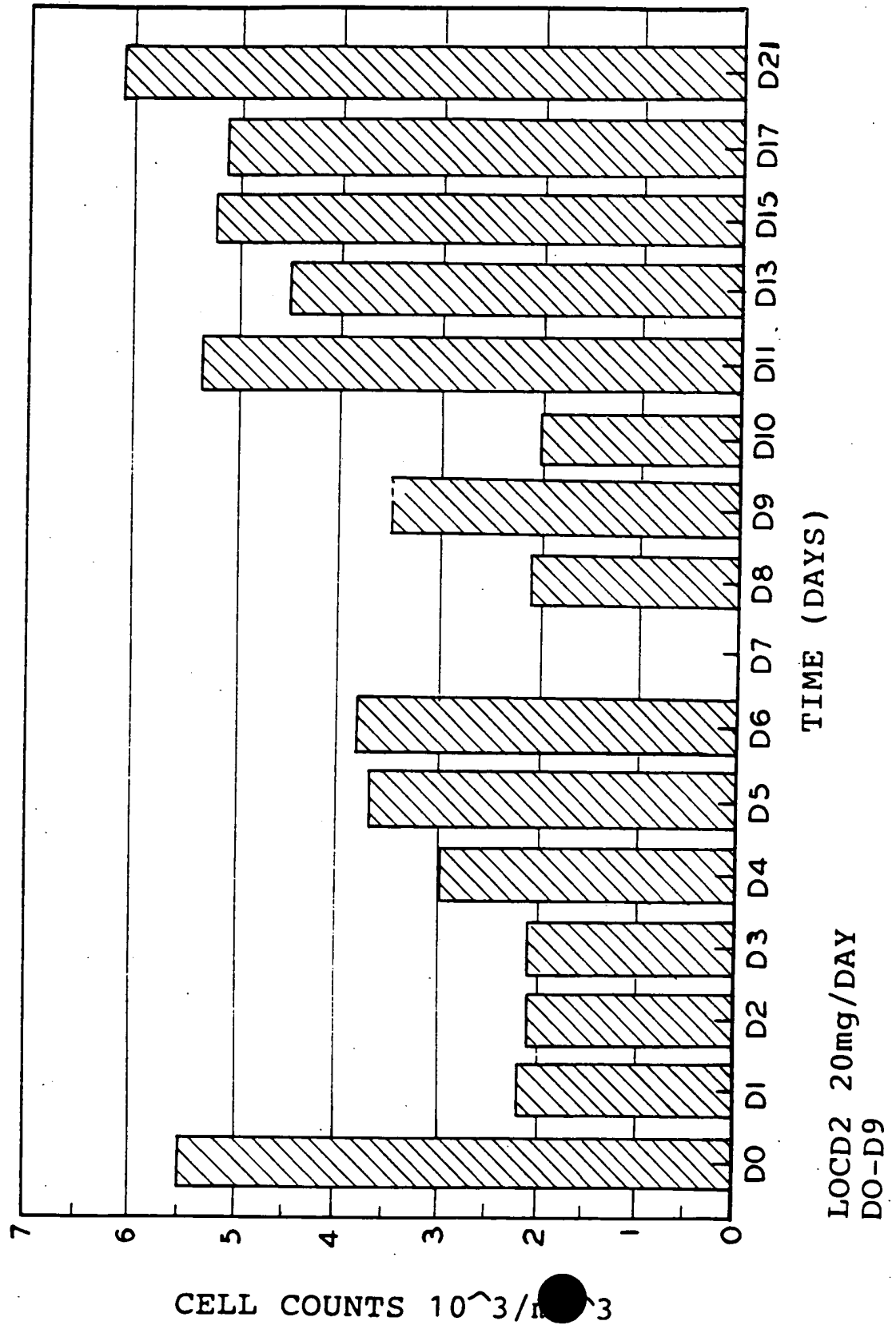
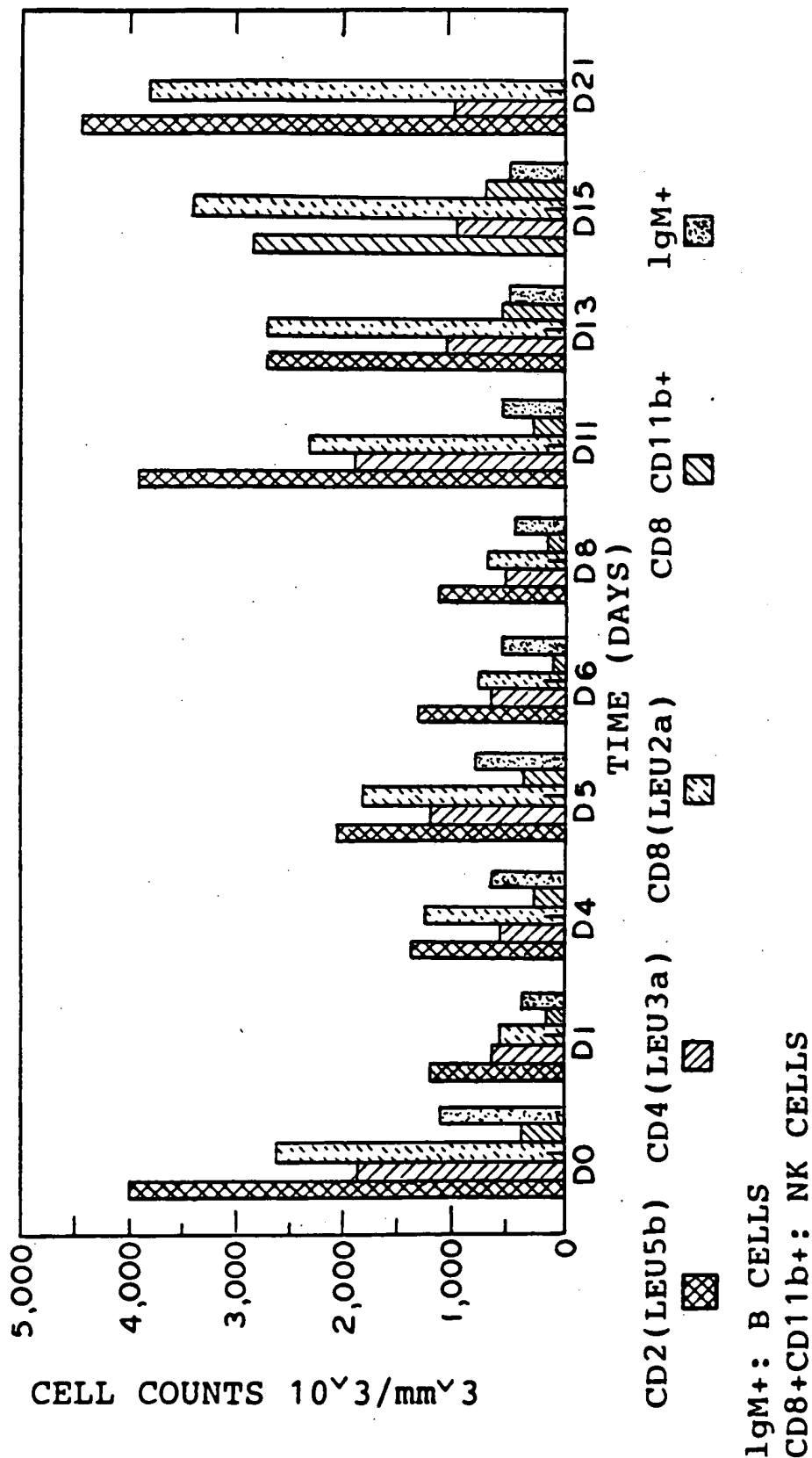


FIG. 13



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FIG. 14

MONKEY #19 (@ AFTER LOCD2 10 DAYS

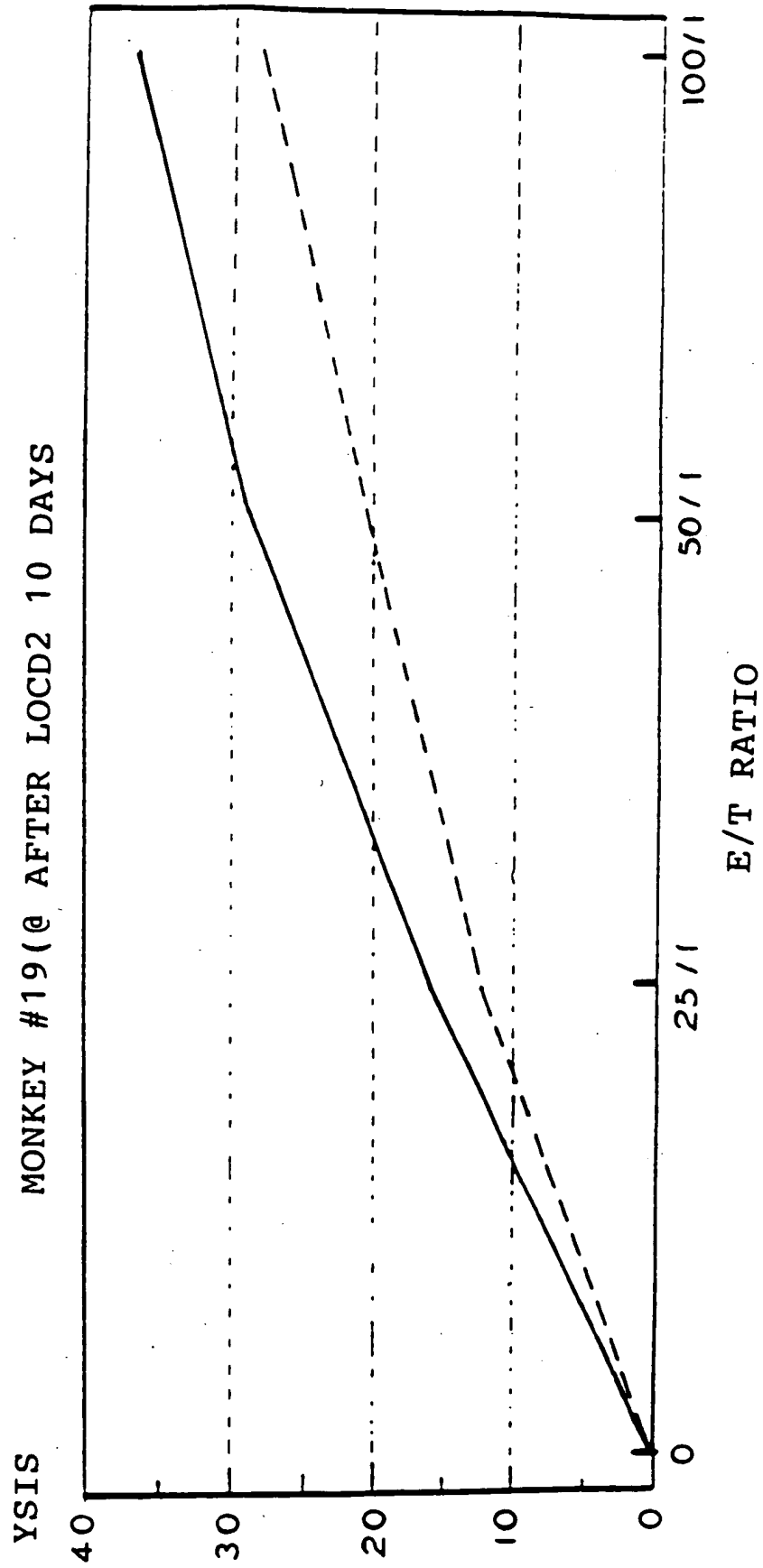
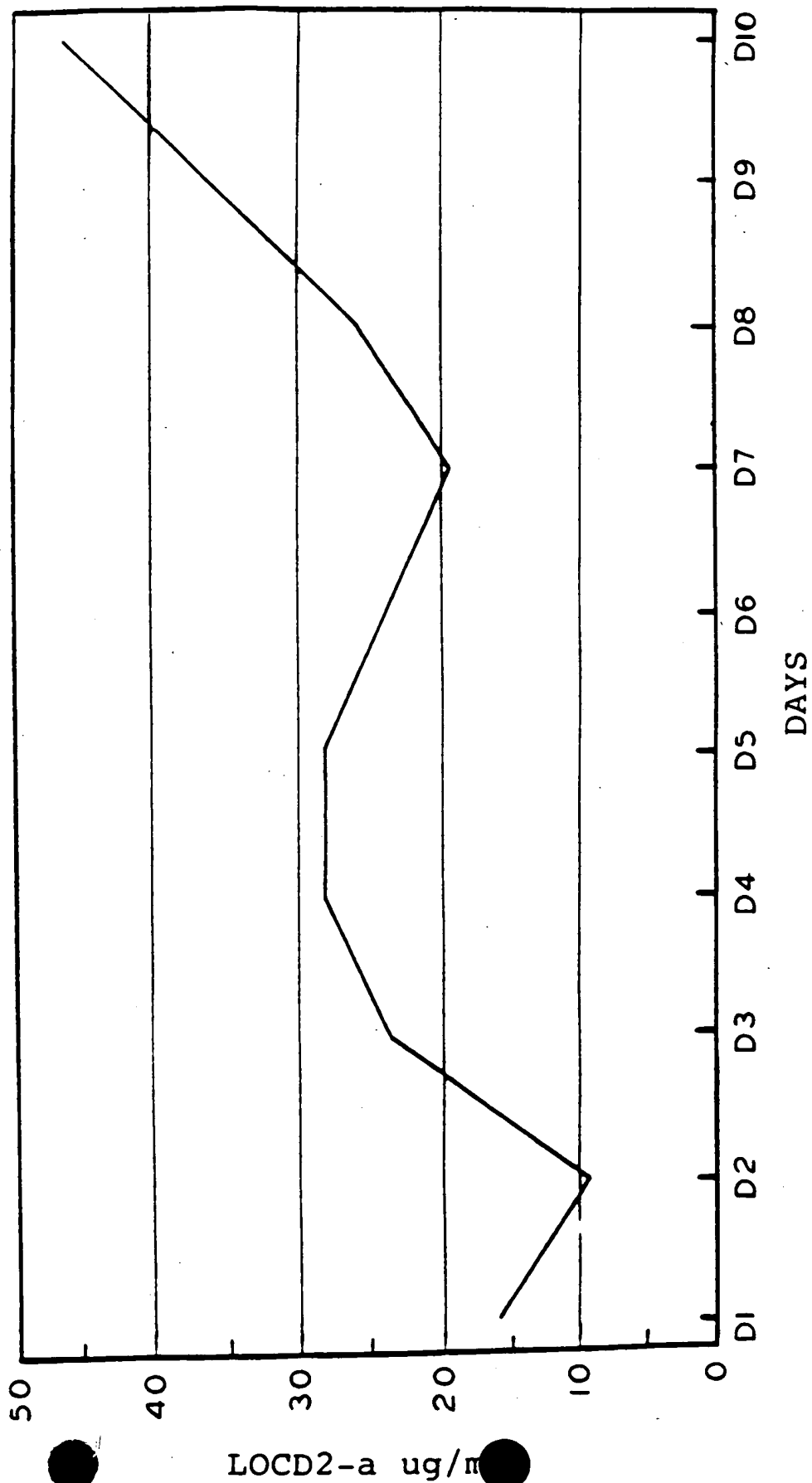


FIG. 15

CYNOMOLGUS MONKEY 1992



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FIG. 17A

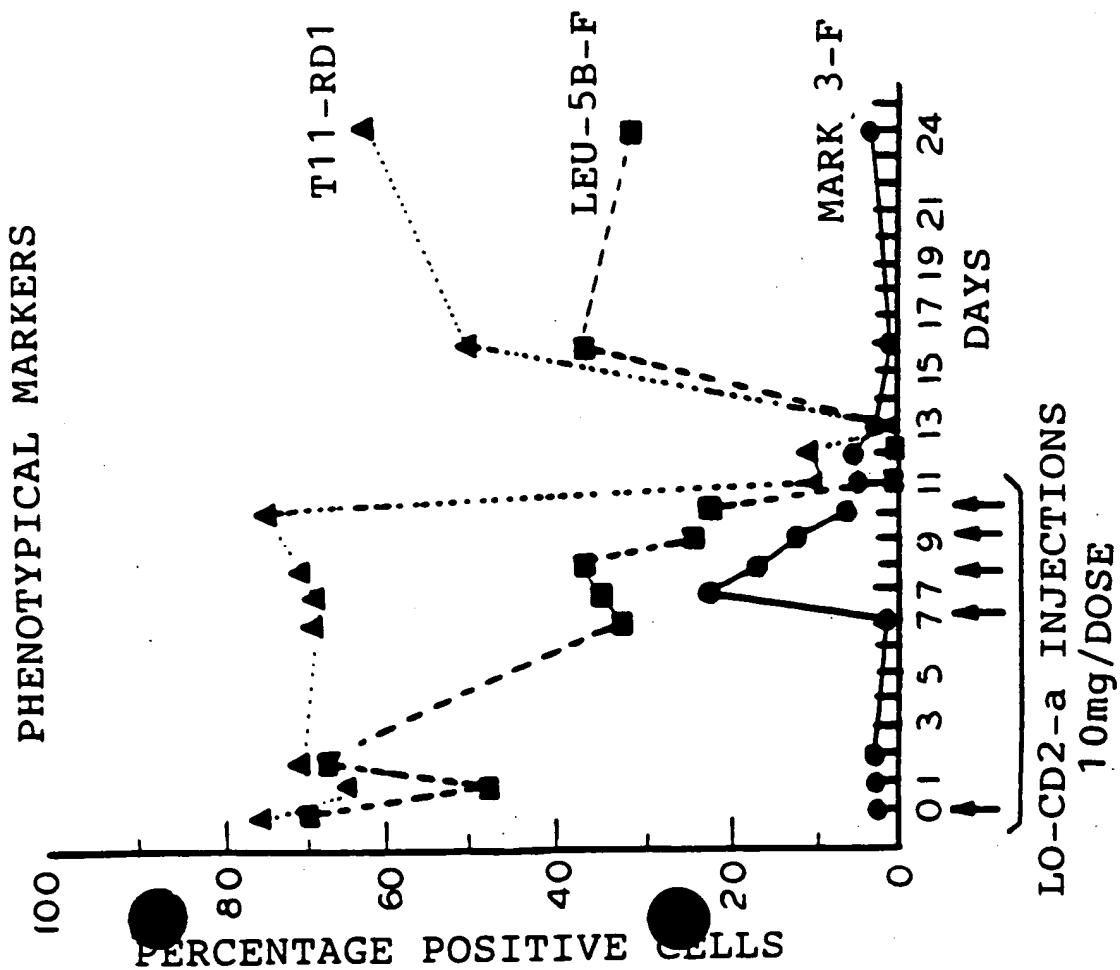


FIG. 17B

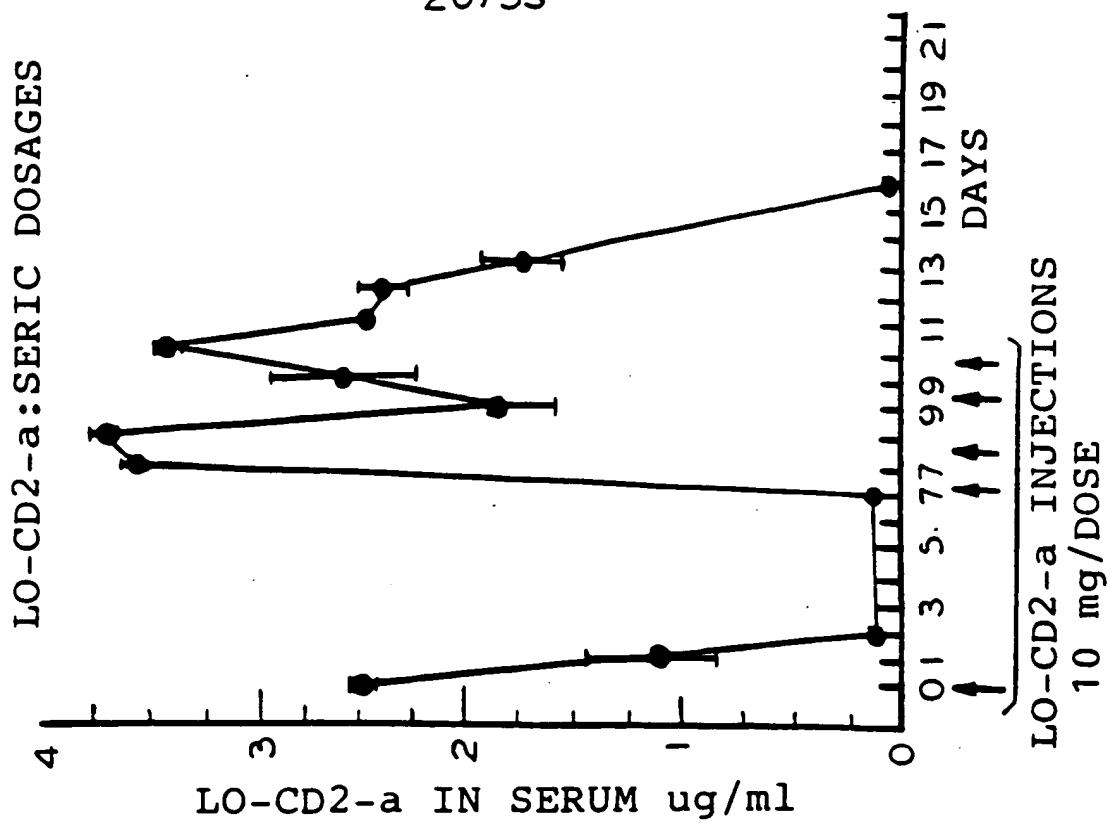


FIG. 18A

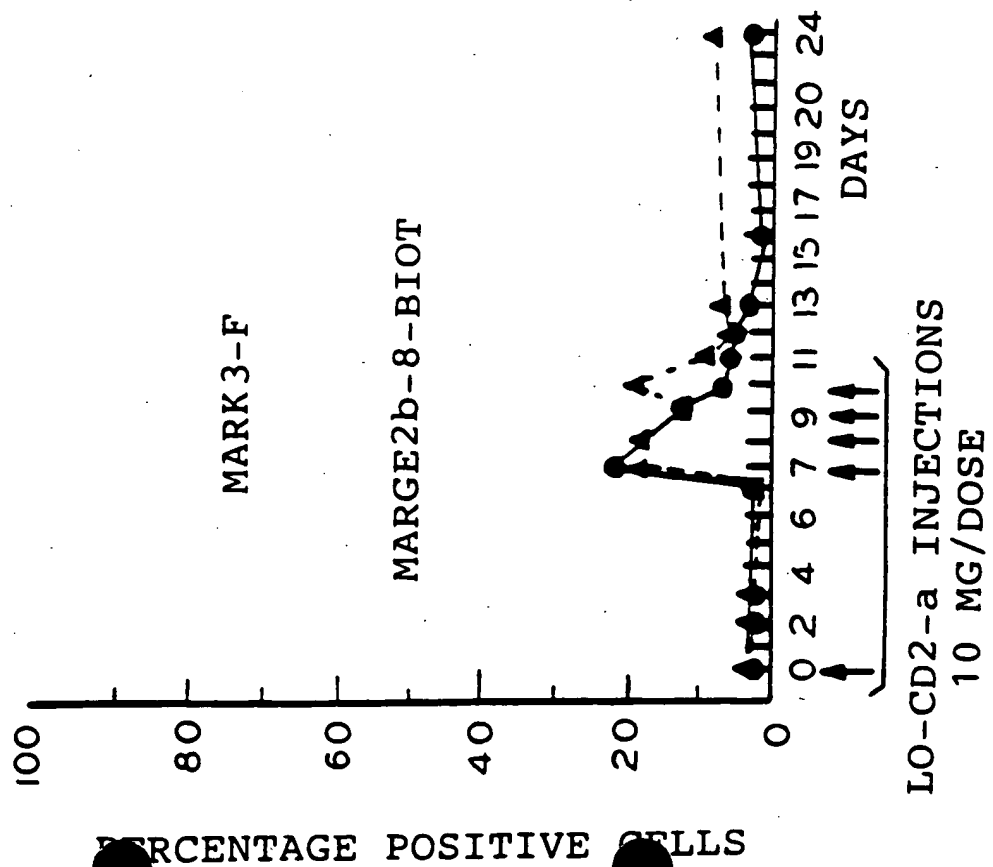
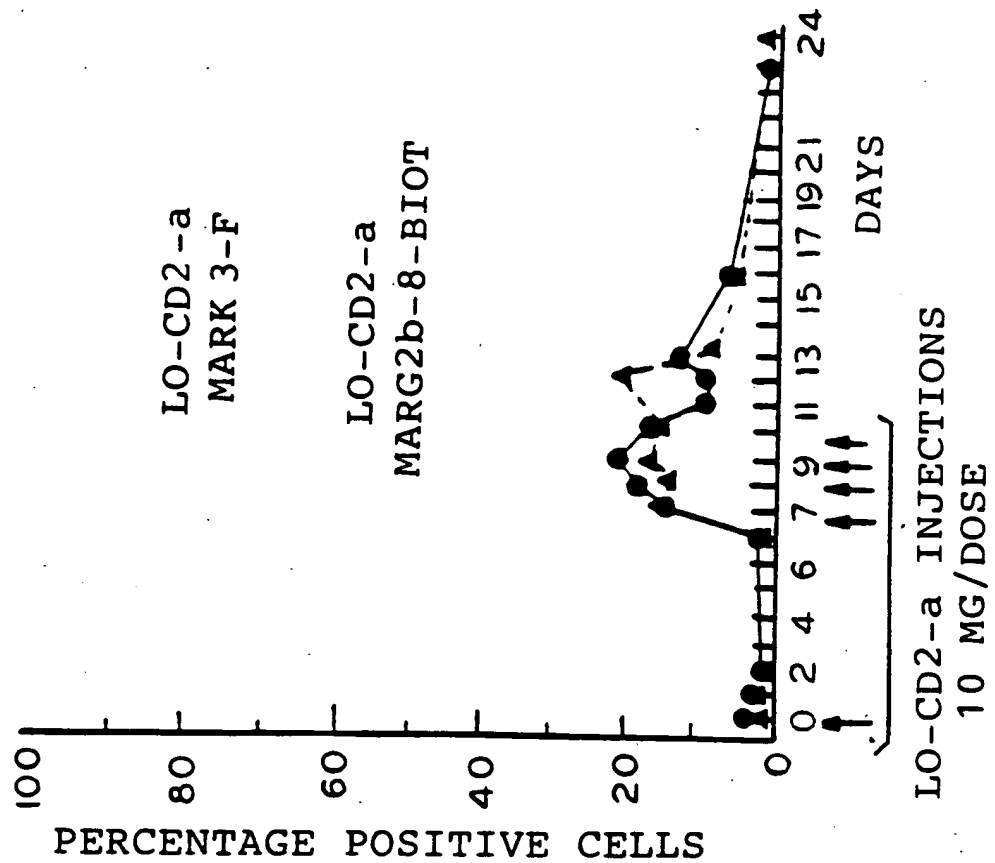


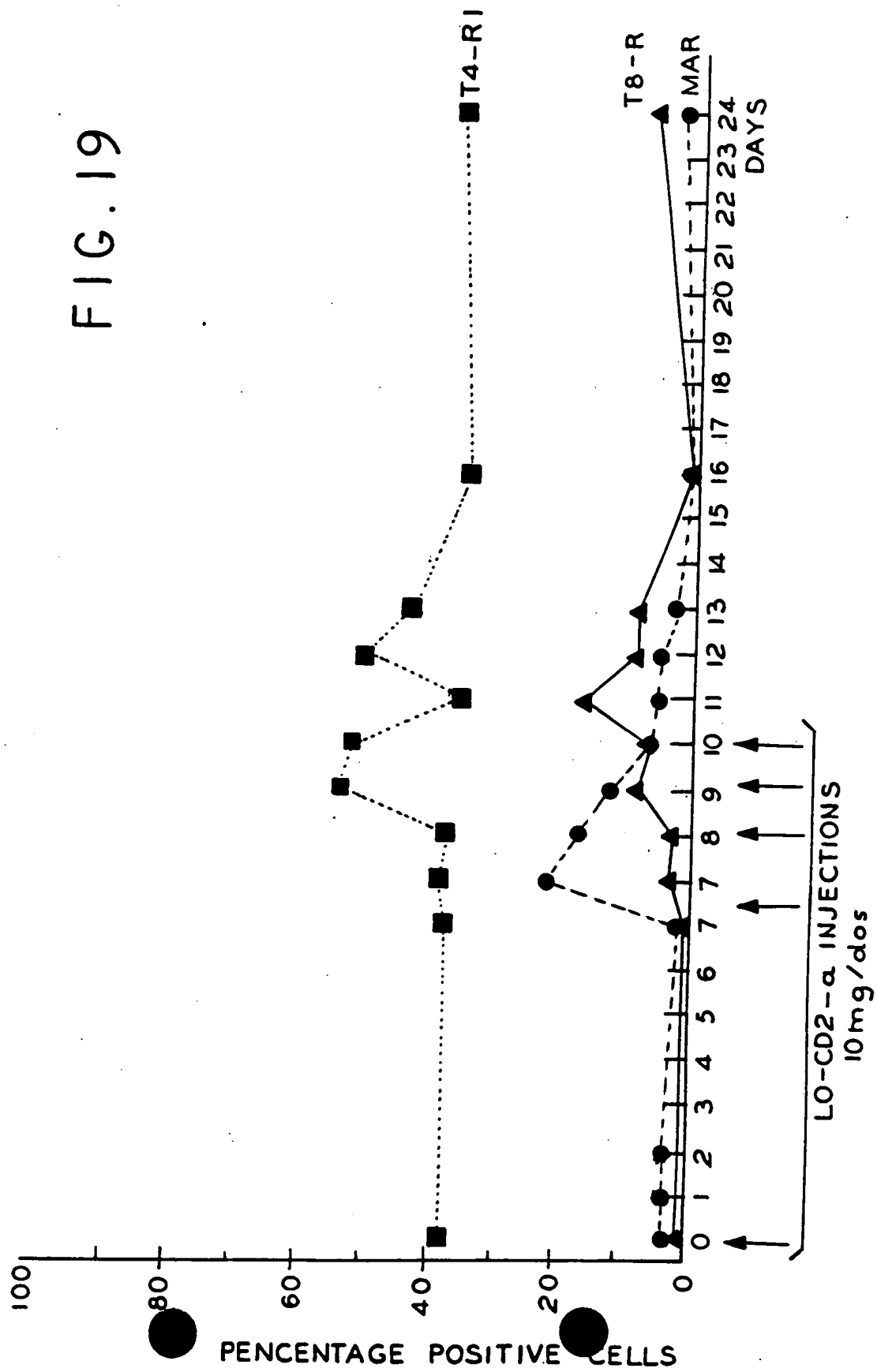
FIG. 18B



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FIG. 19



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FIG. 20

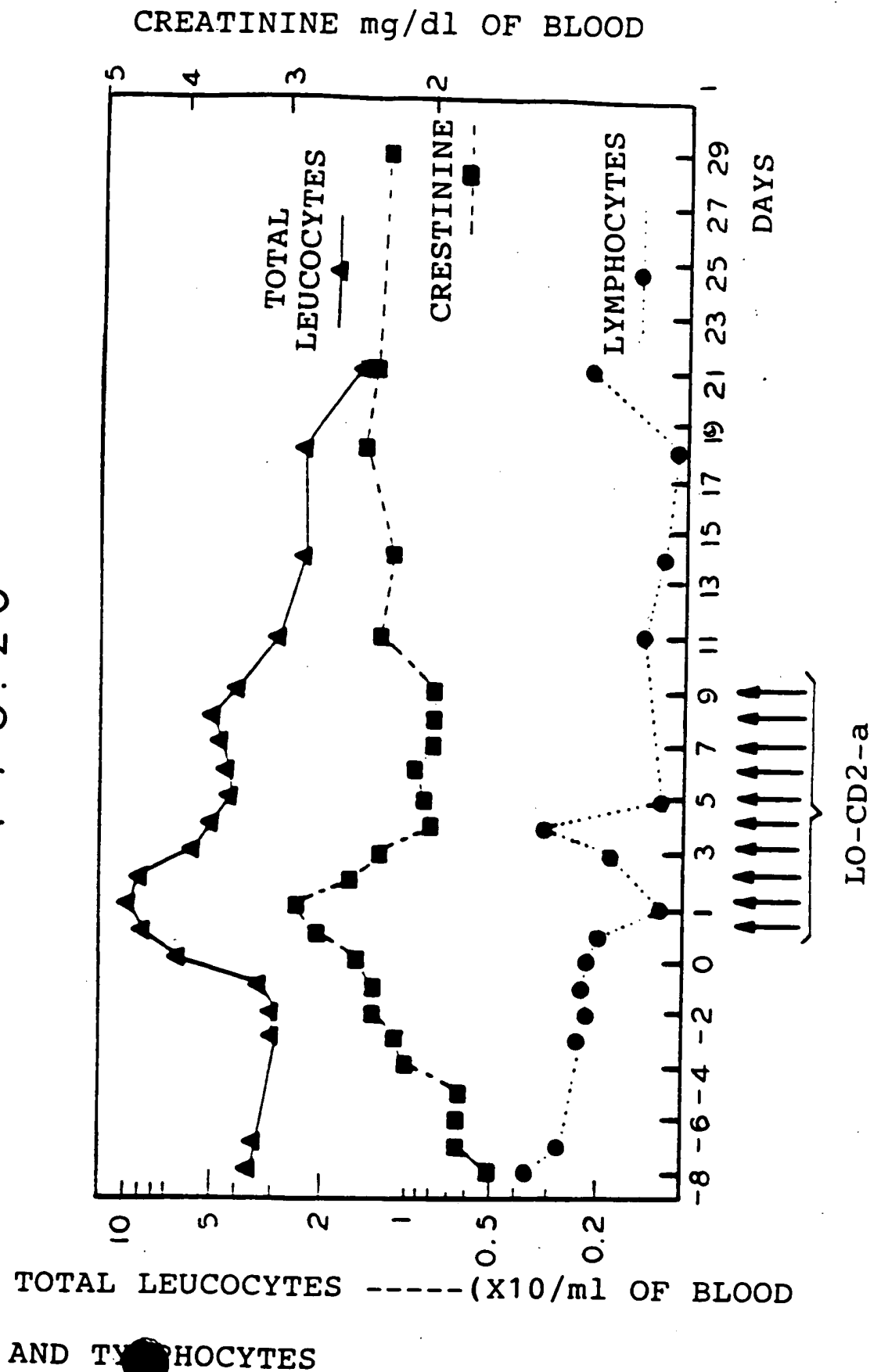
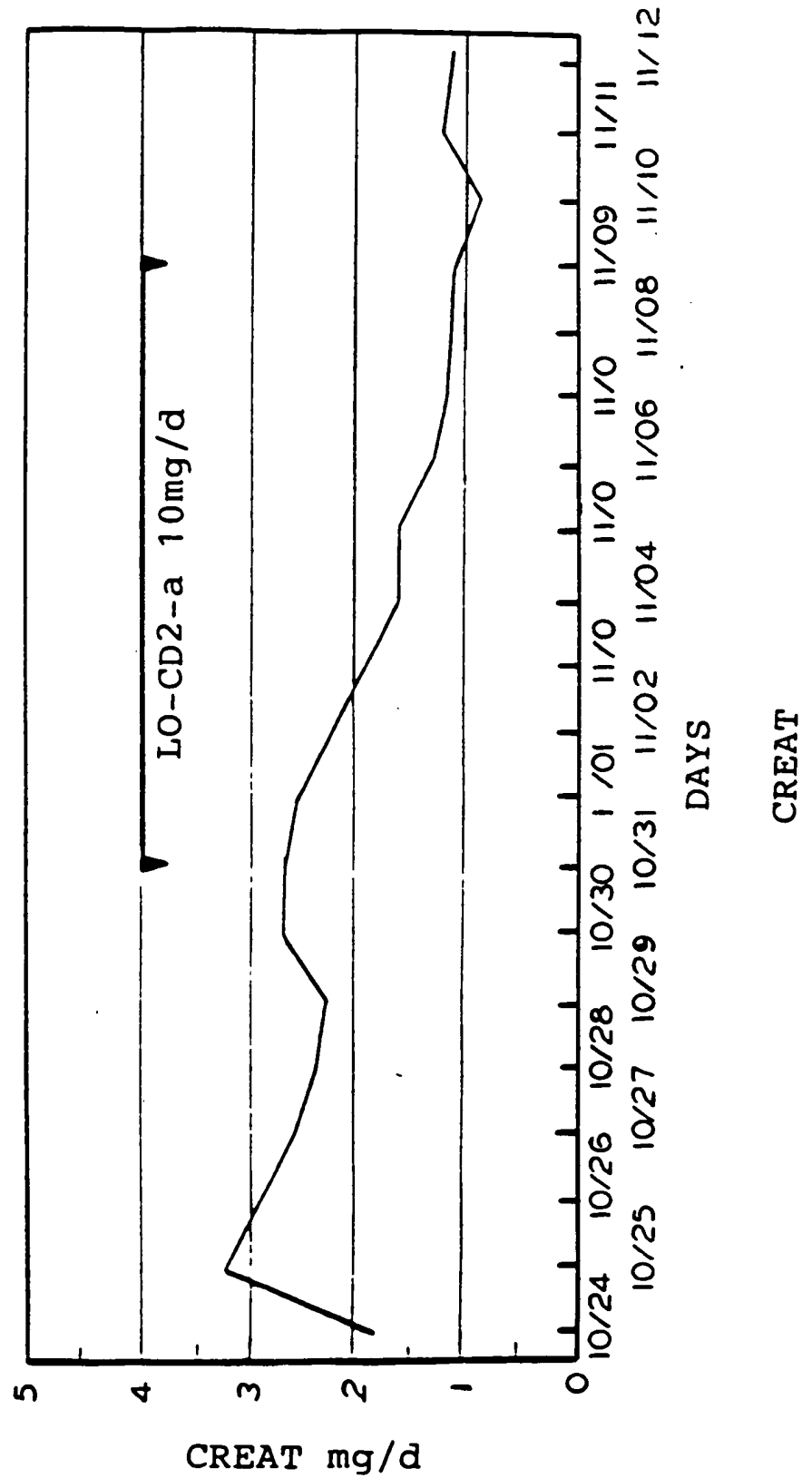


FIG. 22



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FIG. 23

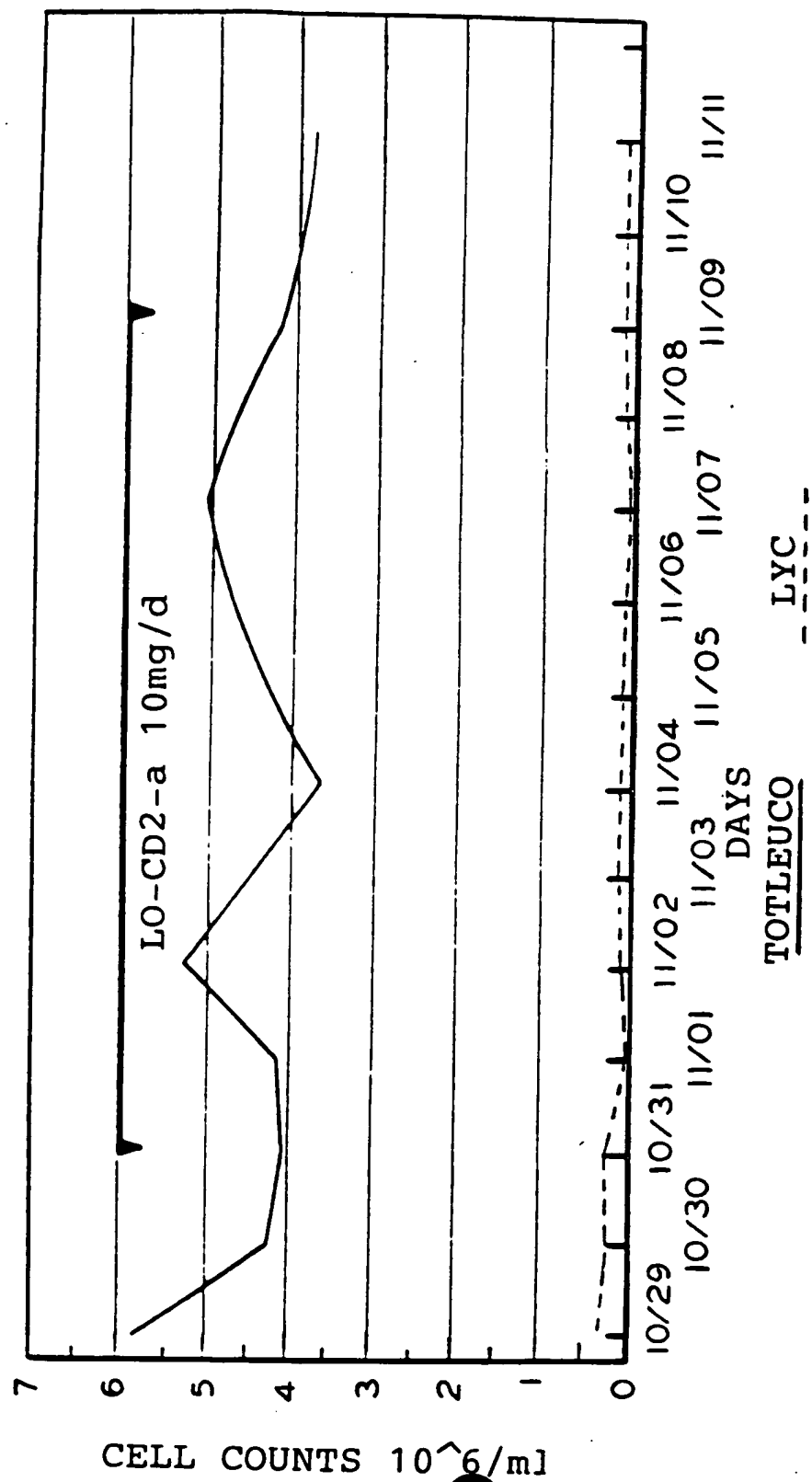
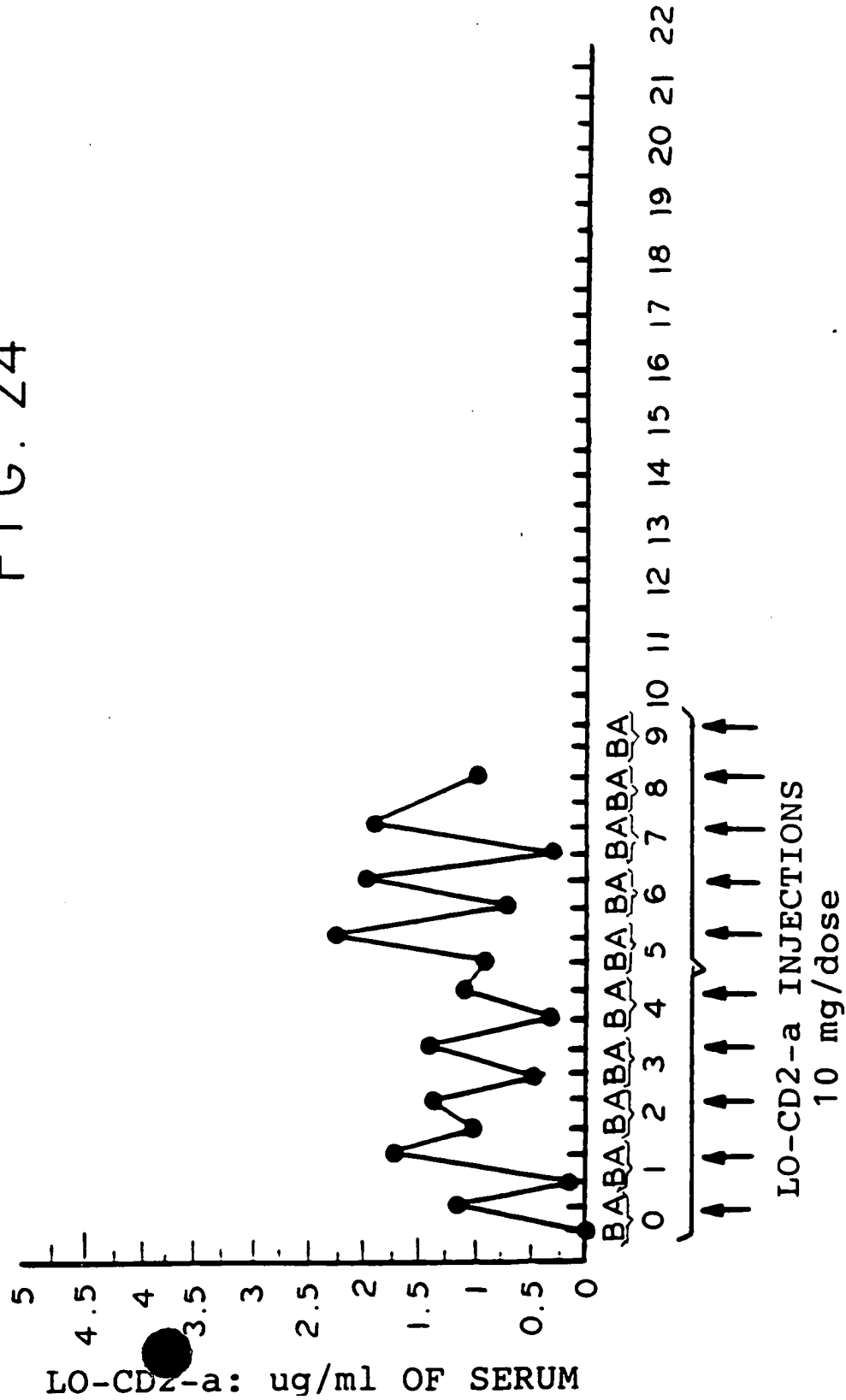
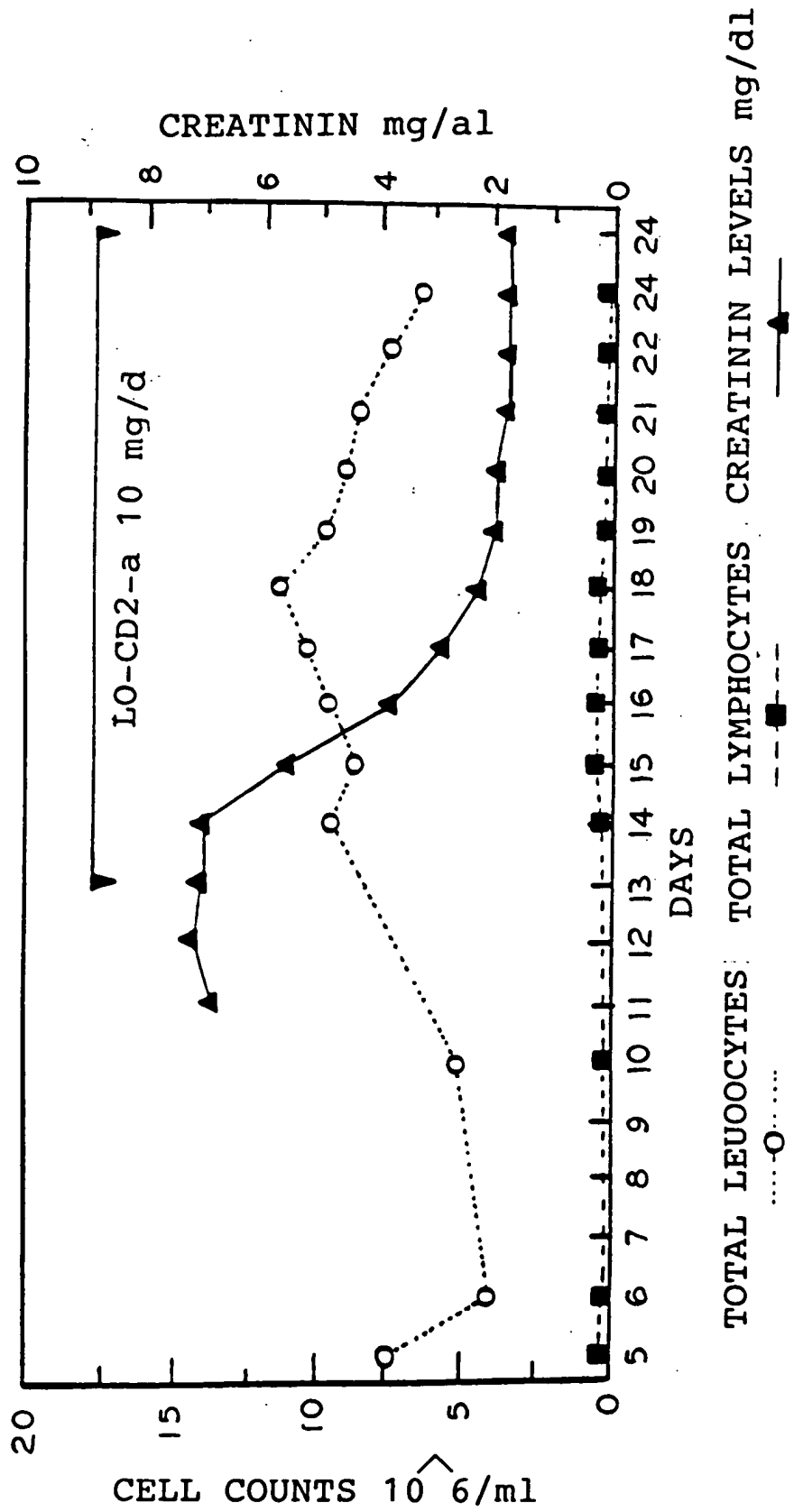


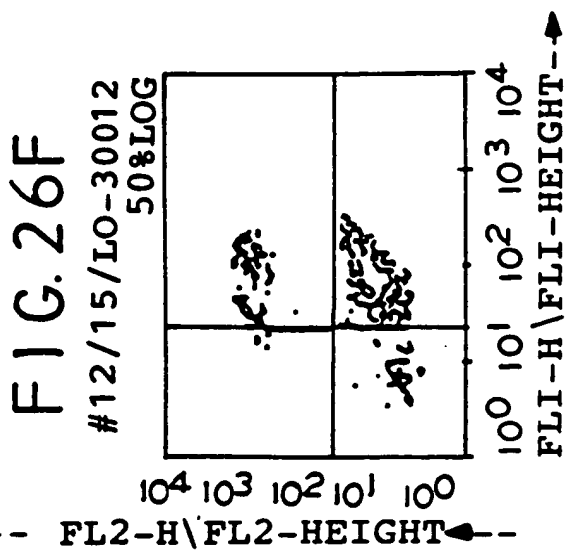
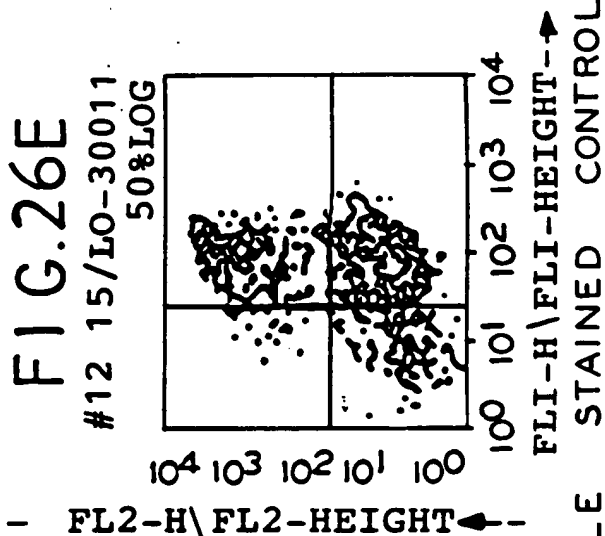
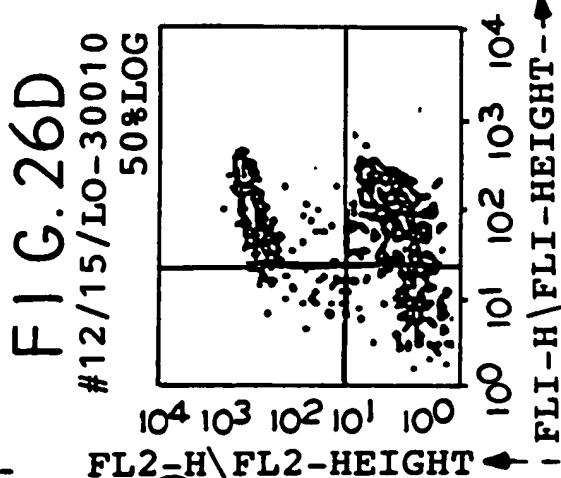
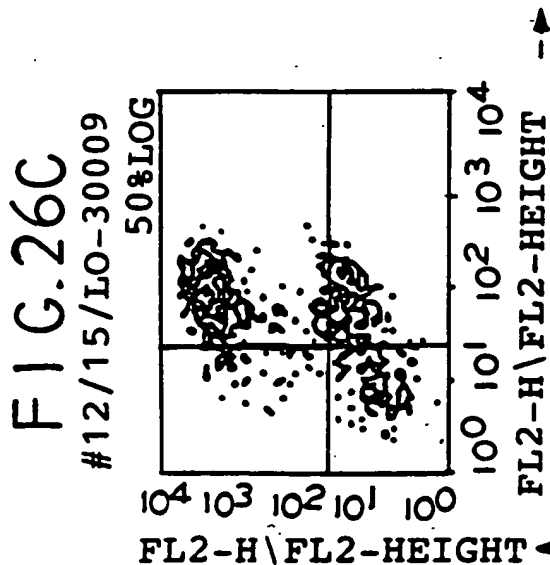
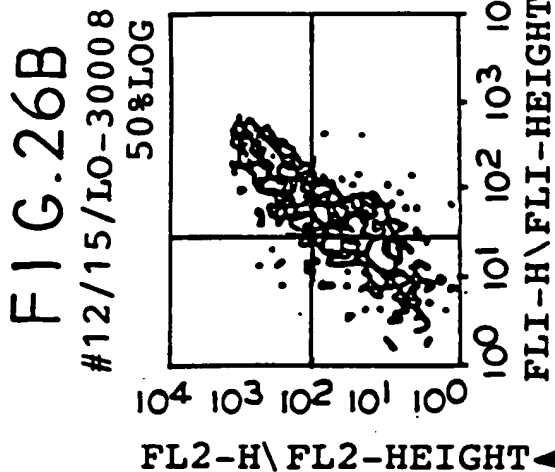
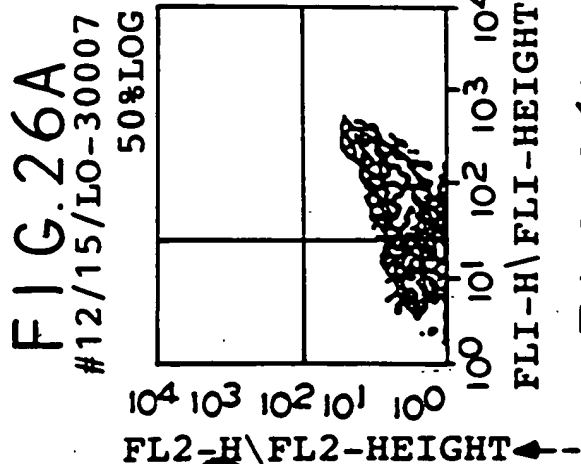
FIG. 24



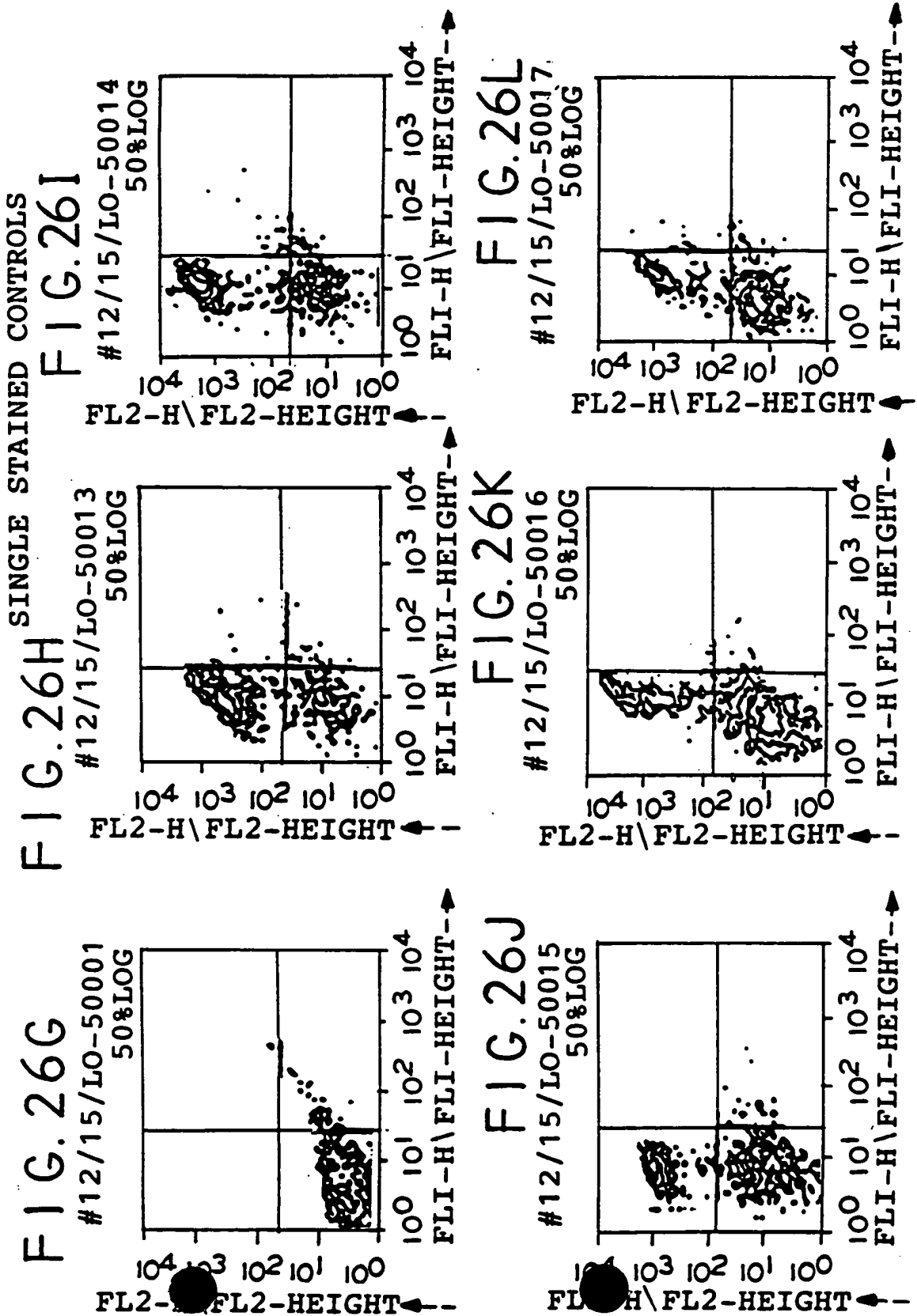
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FIG. 25





SINGLE STAINED CONTROLS



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FIG. 27A

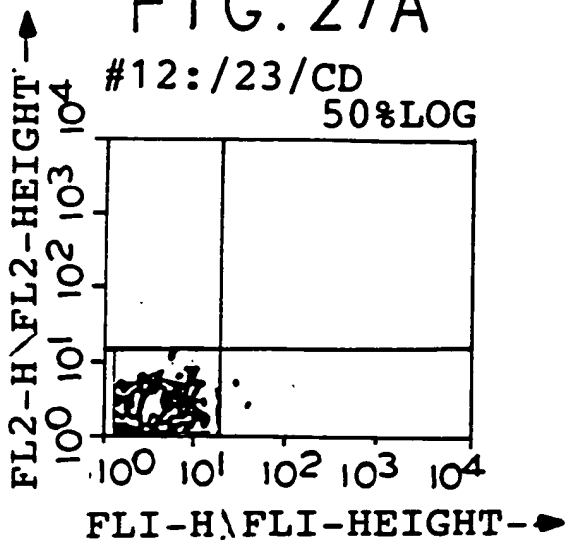


FIG. 27B

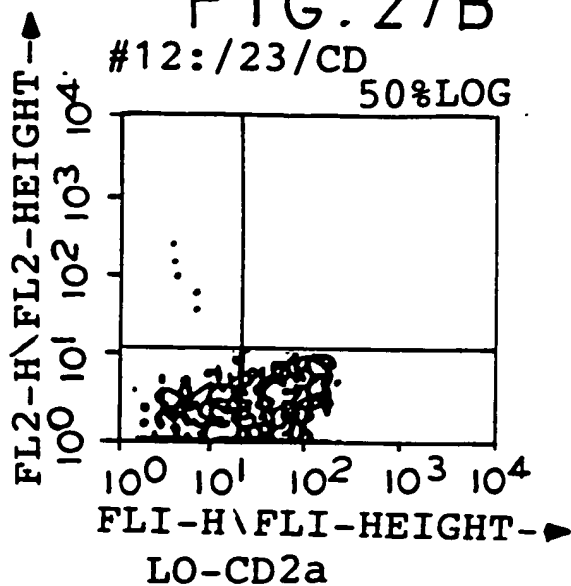


FIG. 27C

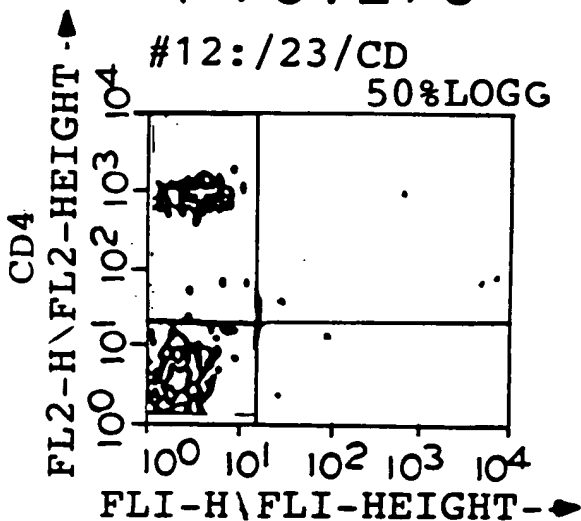


FIG. 27D

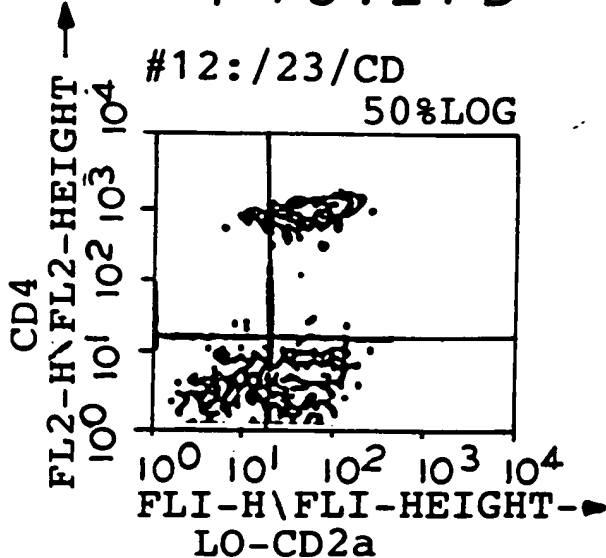


FIG. 27E

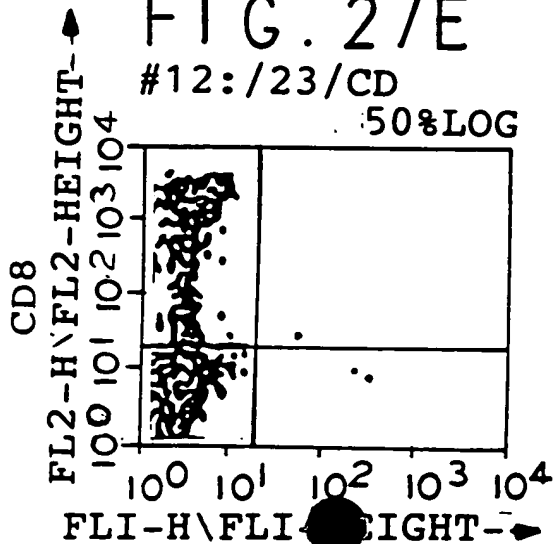
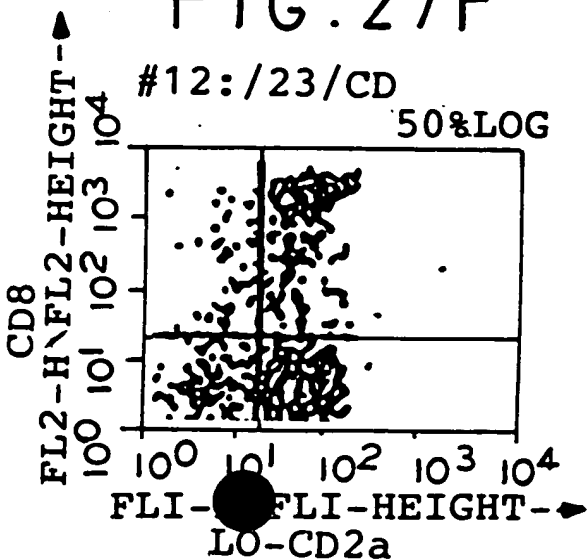


FIG. 27F



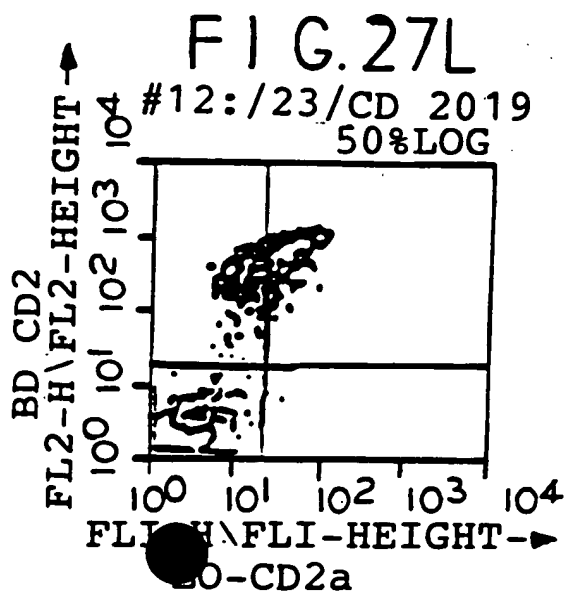
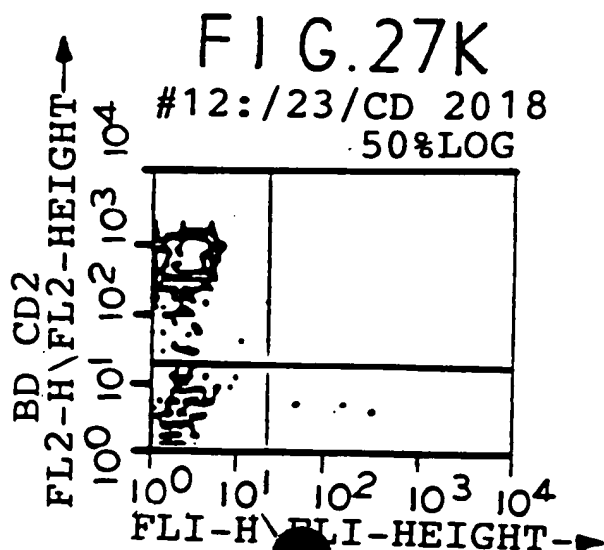
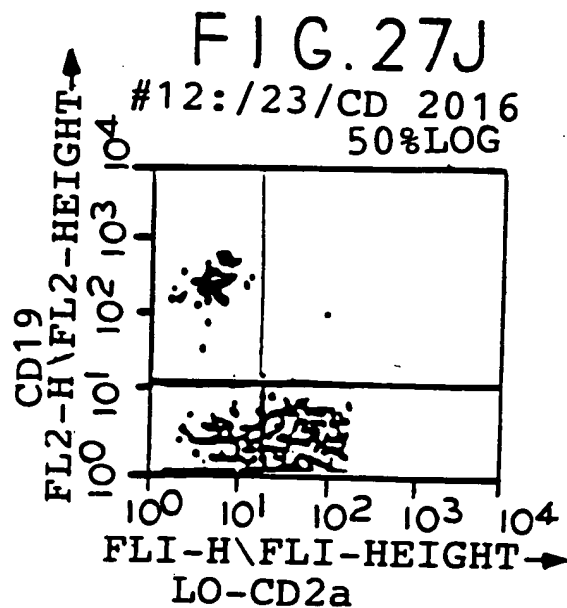
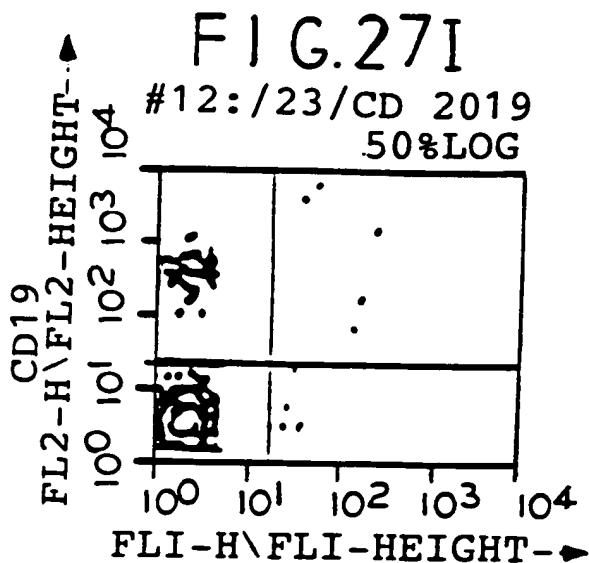
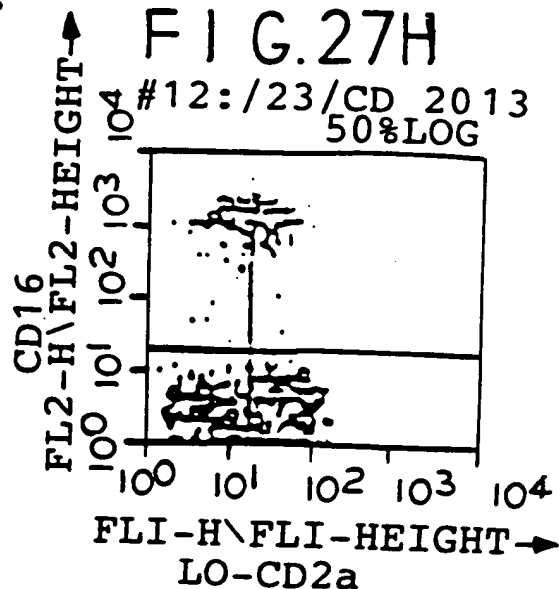
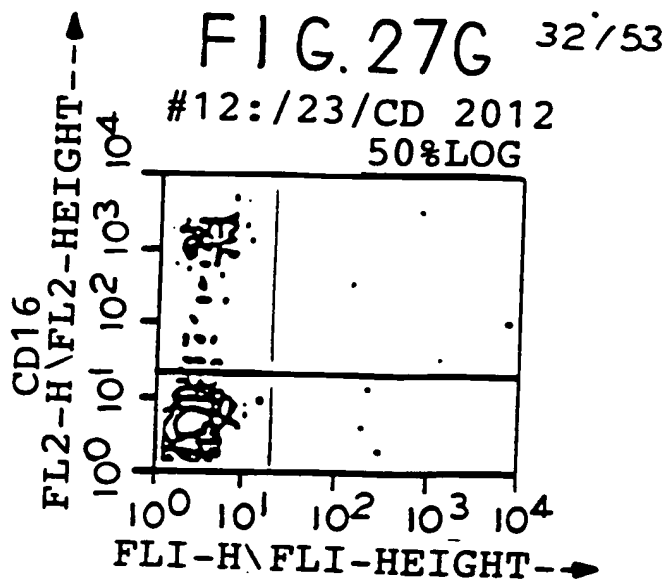


FIG. 28A

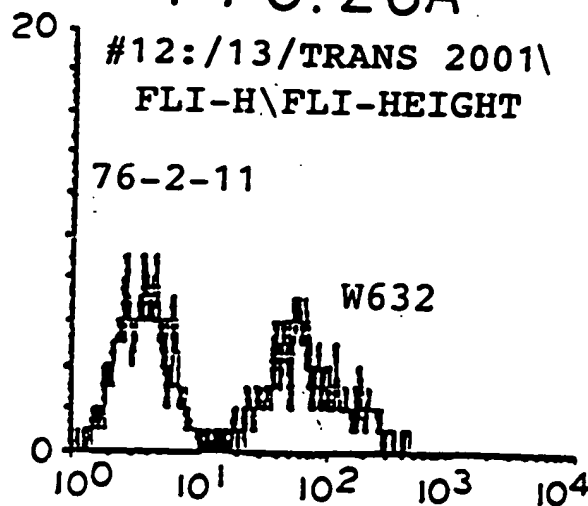


FIG. 28B

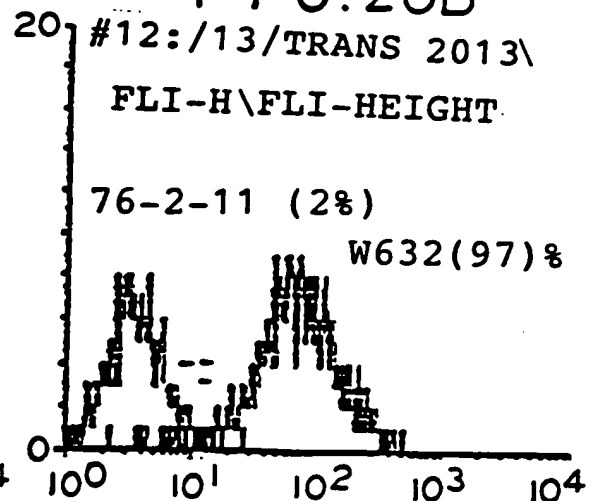


FIG. 28C

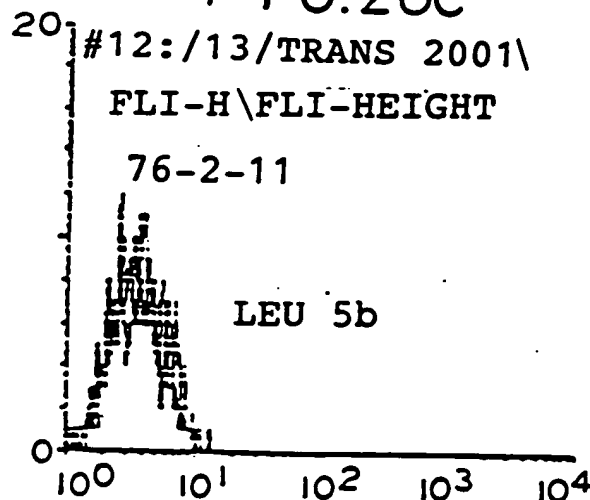


FIG. 28D

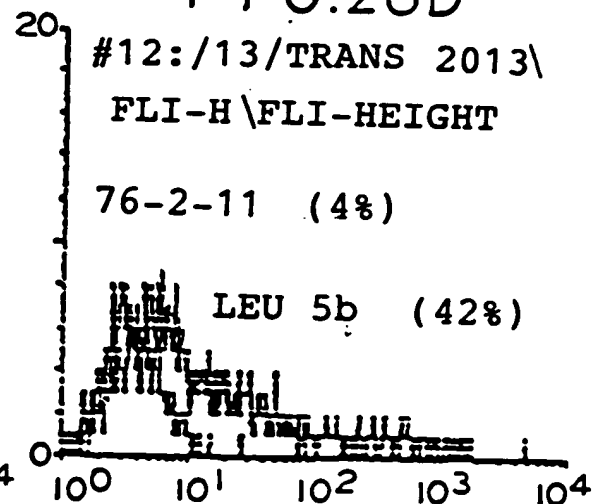


FIG. 28E

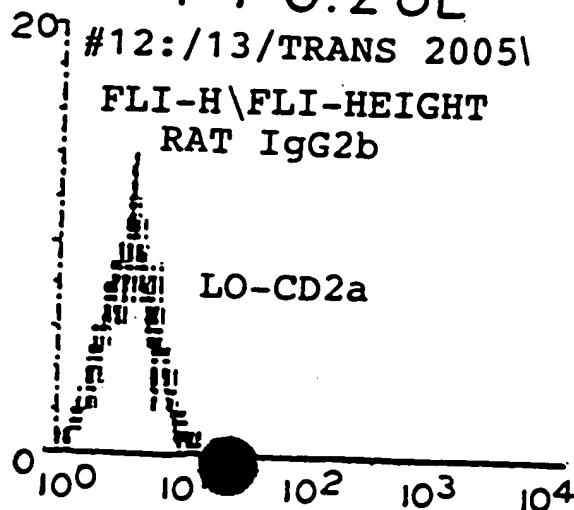
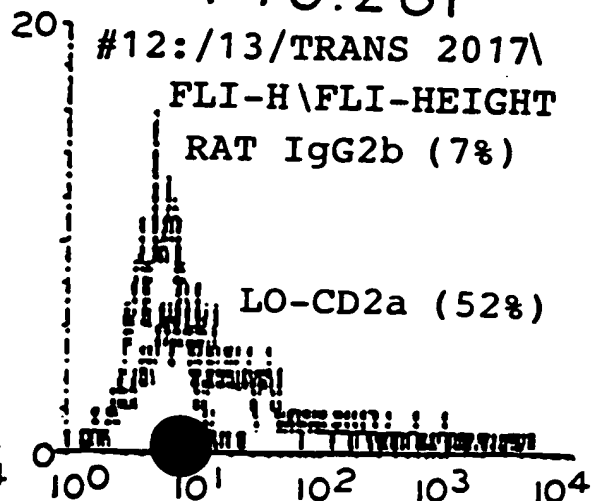


FIG. 28F



```

      10      20      30
    *   *   *   *   *   *   *
  ATGATGAGTCCTGTCCAGTCCCTGTTTCTGTTATT
    M  M  S  P  V  Q  S  L  F  L  L  L

      110     120     130
    *   *   *   *   *   *   *
  GACTGCCCATGTTGGCTGTCCATGTGTGGTAAGGC

      210     220     230
    *   *   *   *   *   *   *
  ATAGGATTTGTGCTAAGAGGATTCTAATGTAGATG

      310     320     330
    *   *   *   *   *   *   *
  TTAAAAATCACAAAACACACCGGGATCTCACAGGA

      410     420     430
    *   *   *   *   *   *   *
  TATTATAATTTTCAGGAACCAATGGTGATGTTGTGC
                        T  N  G  D  V  V

      510     520     530
    *   *   *   *   *   *   *
  AGTCAGAGTCTCTTACATAGTAGTGGAACACCTA
    S  Q  S  L  L  H  S  S  G  N  T  Y

      610     620     630
    *   *   *   *   *   *   *
  TGGAAATCTGGGGTCCCCAACAGGTTTCAGTGGCAGT
  L  E  S  G  V  P  N  R  F  S  G  S

      710     720     730
    *   *   *   *   *   *   *
  CTGCATGCAATTTACCCATTATCCGTATACGTTTG
    C  M  Q  F  T  H  Y  P  Y  T  F

```

MATCH WITH FIG. 29B

09056072-040798

FIG. 29B

40 50 60 70
 * * * * *
 GCTTTGGATTCTGGGTAAGTAGAGAATGAGTTACA
 L W I L G

140 150 160 170
 * * * * *
 AGGTCCTATTTTCTAAGATGGACACTTGAGATTCC

240 250 260 270
 * * * * *
 AGAAGGTGTATGCCATTTAGGATCTGCAACCGAAT

340 350 360 370
 * * * * *
 AATGAGTAACAAAAAGTAATTCACAAAGATTGGTT

440 450 460 470
 * * * * *
 TGACCCAGACTCCACCTACTTTATTGGCTACCATT
 L T Q T P P T L L A T I

540 550 560 570
 * * * * *
 TTTAAATTGGTTGCTACAGAGGACAGGCCAATCTC
 L N W L L Q R T G Q S

640 650 660 670
 * * * * *
 GGGTCAGGAACAGATTTCACTCAAATCAGTGG
 G S G T D F T L K I S G

740 750 760
 * * * * *
 GAGCTGGGACCAAGCTGGAAGTGA
 G A G T K L E L K>

MATCH WITH FIG. 29A

MATCH WITH FIG. 29C

0095060220404686

FIG. 29C

80 90 100
 * * * * *
 GGACAAGAATGGGGATGGAGGATGAGTTCT

180 190 200
 * * * * *
 ATTACTTGATAATGAGAAATTACAGATGAG

280 290 300
 * * * * *
 TGTTTTGTGAAAAAGCATTTGGTATATTTT

380 390 400
 * * * * *
 GCAAATTTTGCACATAACTTTGTTCTGATC

480 490 500
 * * * * *
 GGACAATCAGTCTCCATCTCTTGCAGGTCA
 G Q S V S I S C R S>

580 590 600
 * * * * *
 CACAGCCGCTAATTTATTTGGTATCCAAAC
 P Q P L I Y L V S K>

680 690 700
 * * * * *
 AGTGGAAGTTGAGGATTTGGGGGTTATTA
 V E A E D L G V Y Y>

MATCH WITH FIG. 29B

09056072-040798

FIG. 30A

10 * * 20 * * 30 * * 40 * *
 ATGAAATGCAGGTGGATCATCTTCTTCTTGATGGCAGTAGCTACAG
 M K C R W I I L F L M A V A T

110 * * 120 * * 130 * * 140 * *
 CACTATCTTGGATTCTTGCAACAGGGTCAACTCAGAAAGTTCAG
 V N S E V Q

210 * * 220 * * 230 * * 240 * *
 TGCAAGGCTTCTGGCTATATATTATAGAACTACTATGTACTGGG
 C K A S G Y I F T E Y Y M Y W

310 * * 320 * * 330 * * 340 * *
 ACGGTAGTATTGATTATGTTGAGAAAGTTCAAAAGAGGCCACACT
 D G S I D Y V E K F K K K A T L

410 * * 420 * * 430 * * 440 * *
 TGAGGACACAGCAACCTATTTTGTGCTAGGGGAAATTCAACTAT
 E D T A T Y F C A R G K F N Y

Match with FIG. 30B

CGATTGCTTACTGGGCCAAGGCACCCCTCGTCACAGTCTCCTCA
R F A Y W G Q G T L V T V S S >

FIG. 3I

	FR 1	*	*	20	CDR 1	30	40	FR 2	*
Rat Lo-CD2a Vk	DVVL	TQ	TPPT	LLATIGQSVS	ISCRSSQSL	L	HSSGNTYLNW	LLQRTGQSPQ	
Humanized Vk	---	M---	S---	--V-L--PA-	-----	-----	-----	-----P-----	
Human HUM5400 Vk	---	M---	S-LS	-PV-L--PA-	-	-V	Y-D---	H---FQ--P----	R

	CDR 2	60	70	FR 3	80	90	CDR 3	100
Rat LO-CD2a Vk	PLIYLVSKLE	SGV	PNRFSGS	GS	GTDFTLKI	SGVEAEDLGV	YYCMQFTHYP	
Humanized Vk	-----	---	D---	-----	-----	-----V--	-----	
HumanHUM5400 Vk	R---	K--NRD	----	D-----	-----	-R-----V--	-----G--W-	

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	FR 4	110
Rat LO-CD2a Vk	YTFGAGTKLE	LK
Humanized Vk	-----Q-----	I-
HumanHUM5400 Vk	-----Q-----	I-

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FIG. 32A

10 20 30
* * * * *
AAGCTTCATGATGAGTCCTGTCCAGTCCTTGTTTC
M M S P V Q S L F

110 120 130
* * * * *
GAGTTCTGACTGCCCATGTTGGCTGTCCATGTGTG

210 220 230
* * * * *
AGATGAGATAGGATTTGTGCTAAGAGGATTCTAAT

310 320 330
* * * * *
ATATTTTTTTAAAAATCACAAACACACCGGGATCT

410 420 430
* * * * *
TCTGATCTATTATAATTCAGGAACCAATGGTGAT
T N G D

510 520 530
* * * * *
CAGGTCAAGTCAGAGTCTCTTACATAGTAGTGGA
R S S Q S L L H S S G

610 620 630
* * * * *
TCCAAACTGGAATCTGGGGTCCCCGACAGGTTTCAG
S K L E S G V P D R F S

710 720 730
* * * * *
TTTATTACTGCATGCAATTTACCCATTATCCGTAC
V Y Y C M Q F T H Y P Y

TGGATCC

MATCH WITH FIG. 32B

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FIG. 32B

40 50 60 70
 * * * * *
 TGTATTGCTTTGGATTCTGGGTAAGTAGAGAATG
 L L L L W I L G>

140 150 160 170
 * * * * *
 GTAAGGCAGGTCCTATTTTCTAAGATGGACACTTG

240 250 260 270
 * * * * *
 GTAGATGAGAAGGTGTATGCCATTTAGGATTTGCA

340 350 360 370
 * * * * *
 CACAGGAAATGAGTAACAAAAAGTAATTCACAAAG

440 450 460 470
 * * * * *
 GTTGTGATGACCCAGAGTCCACCTTCATTATTGGT
 V V M T Q S P P S L L V

540 550 560 570
 * * * * *
 ACACCTATTTAAATTGGTTGCTACAGAGGCCAGGC
 N T Y L N W L L Q R P G

640 650 660 670
 * * * * *
 TGGCTCAGGGAGTGGAACAGATTTCACTCAAAA
 G S G S G T D F T L K

740 750 760 770
 * * * * *
 ACGTTGGACAAGGAACCAAGCTCAAAATCAAACG
 T G Q G T K L E I K>

MATCH WITH FIG. 32A

MATCH WITH FIG. 32C

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0905607 040798

MATCH WITH FIG. 32B

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FIG. 32C

80 90 100
* * * * *
AGTTACAGGACAAGAATGGG GATGGAGGAT

180 190 200
* * * * *
AGATTCCATTACTTGATAATGAGAAATTAC

280 290 300
* * * * *
ACCAATTGTTTGTGAAAAAGCATTTGGT

380 390 400
* * * * *
ATTGGTTGCAAATTTTGCACATAACTTTGT

480 490 500
* * * * *
AACCTTGGGACAACCAGCTTCCATCTCTTG
T L G Q P A S I S C>

580 590 600
* * * * *
CAATCTCCACAGCCGCTAATTTATTTGGTA
Q S P Q P L I Y L V>

680 690 700
* * * * *
TCAGTGGAGTGGAAGCTGAGGATGTGGGGG
I S G V E A E D V G>

780 790 800
* * * * *
TGAGTAGAATTTAAACTTCTTCCTCAGT

FIG. 34A

10 20 30
 * * * * * * *
 AAGCTTCATGAAATGCAGGTGGATCATCCTCTTCT
 M K C R W I I L F

110 120 130
 * * * * * * *
 ACAGTGACACTATCTTTGGATTTCTTTCAACAGGG

210 220 230
 * * * * * * *
 GGTCTCCTGCAAGGCTTCTGGATACACCTTCACCG
 V S C K A S G Y T F T

310 320 330
 * * * * * * *
 CCTGAAGACGGTAGTATTGATTATGTTGAGAAGTT
 P E D G S I D Y V E K F

410 420 430
 * * * * * * *
 TGACCTCTGACGACACGGCCGTGTATTACTGTGCG
 L T S D D T A V Y Y C A

510 520 530
 * * * * * * *
 TGAGTCTTTACAACCTCTCTCTTCTATTTCAGCTTA

610 620 630
 * * * * * * *
 AGGGACACCTTGGGAGTCAGAAAGGGTCATTGGGA

MATCH WITH FIG. 34B

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FIG. 34B

40 50 60 70
 * * * * *
 TGATGGCAGTAGCTACAGGTAAGGCACTCCCAAGTC
 L M A V A T G>

140 150 160 170
 * * * * *
 GTCAACTCACAGGTGCAGCTGGTGCAGTCTGGGGCT
 V N S Q V Q L V Q S G A

240 250 260 270
 * * * * *
 AGTACTATATGTACTGGGTGCGACAGGCCCTGGAC
 E Y Y M Y W V R Q A P G

340 350 360 370
 * * * * *
 TAAGAAAAAGGTCACCCTGACCGCTGACACGTCCTC
 K K K V T L T A D T S S

440 450 460 470
 * * * * *
 AGAGGAAAGTTTAATTATAGTTTTGCTTACTGGGGC
 R G K F N Y R F A Y W G

540 550 560 570
 * * * * *
 AATAGATTTTACTGCATTTGTTGGGGGGGAAATGTG

640 650 660 670
 * * * * *
 GCCCGGGCTGATGCAGACAGACATGCTCAGCTCCCG

MATCH WITH FIG. 34A

MATCH WITH FIG. 34C

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FIG. 34C

80 90 100
 * * * * *
 CTAAACTTGAGAGATCATA CACTTGGGAG

180 190 200
 * * * * *
 GAGGTGAAGAAGCCTGGGG CCTCAGTGAA
 E V K K P G A S V K>

280 290 300
 * * * * *
 AAGGGCTTGAGCTGATGGG AAGGATCGAT
 Q G L E L M G R I D>

380 390 400
 * * * * *
 TAGCACAGCCTACATGGAG CTGAGCAGCC
 S T A Y M E L S S>

480 490 500
 * * * * *
 CAAGGAACCCTGGTCACCG TCTCCTCAGG
 Q G T L V T V S S>

580 590 600
 * * * * *
 TGTATCTGAATTTTCAGGTC ATGAAGGACT

680 690 700
 * * * * *
 GACTTCATGGCCAGAGATT TATAGGGATC

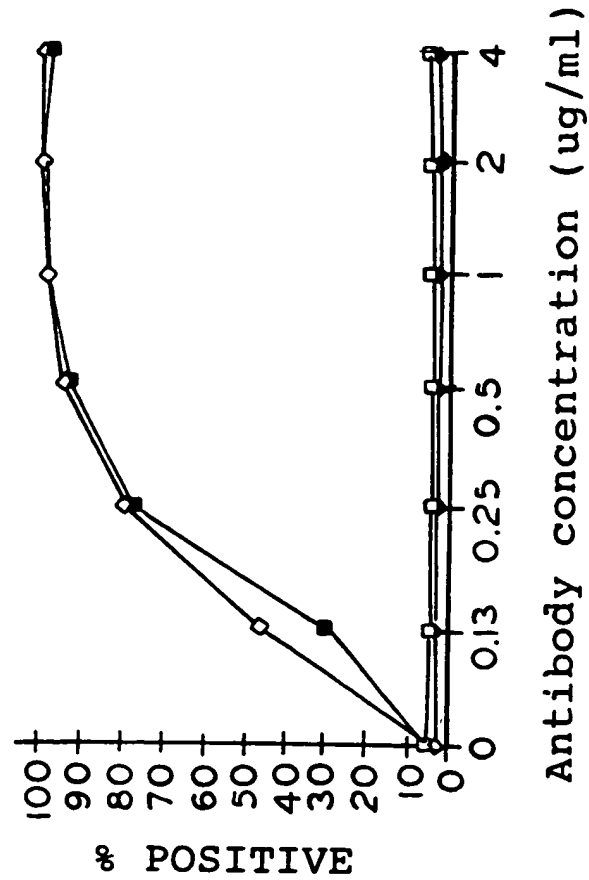
MATCH WITH FIG. 34B

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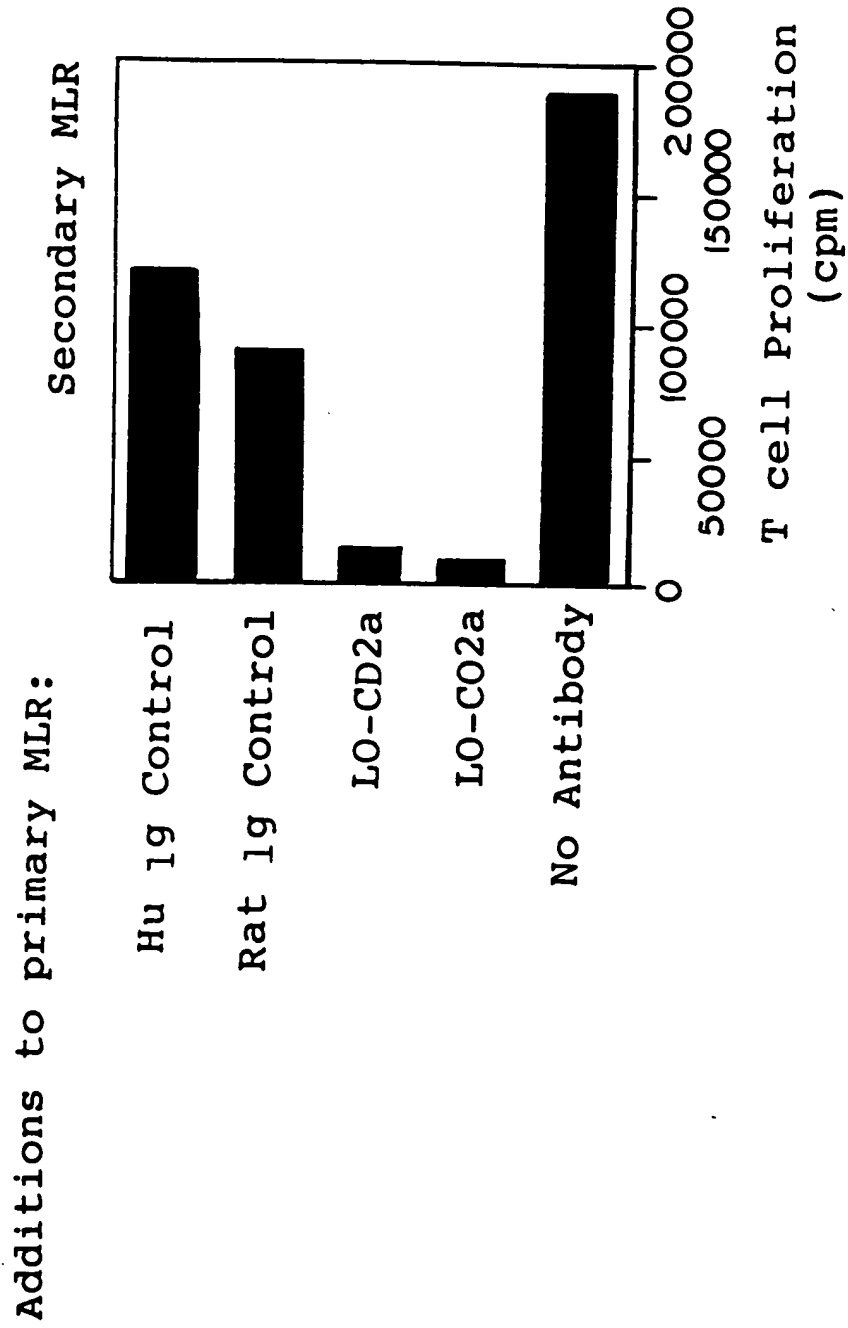
FIG. 35

—●— LO-CD2a
 —○— Rat IgG2b control
 —◆— Human IgG control
 —◇— LO-CO2c Hu



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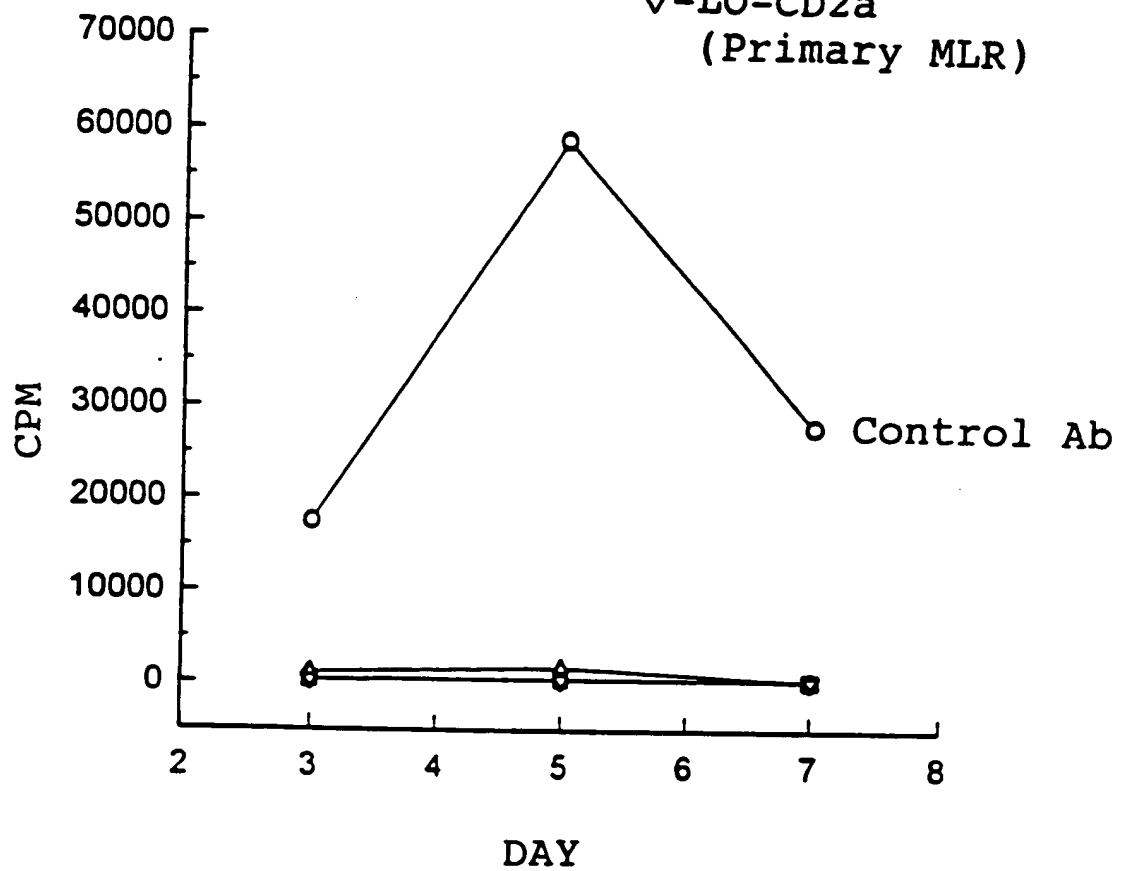
FIG. 36



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FIG. 37

□ -LO-CD2a
△ -Control Ab
(Primary MLR)
▽ -LO-CD2a
(Primary MLR)



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FIG. 38A

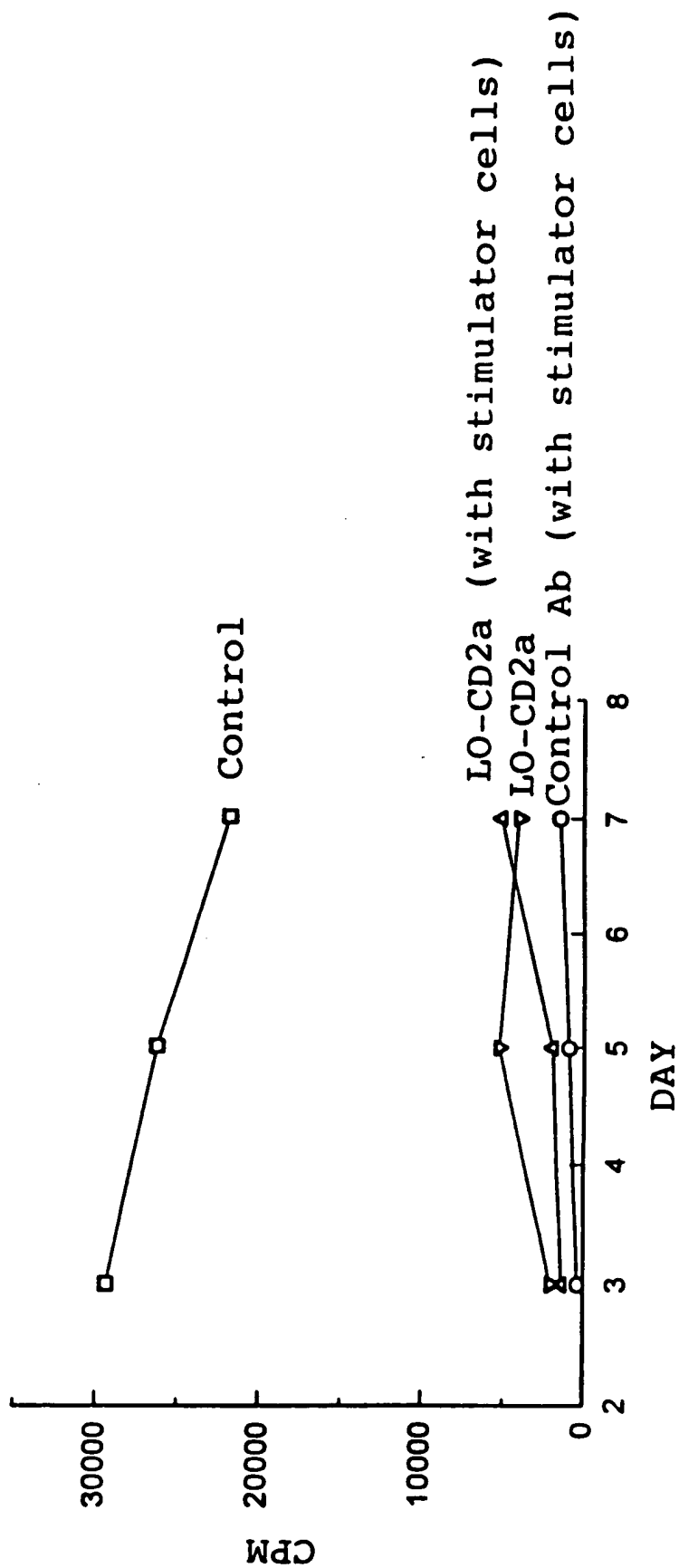
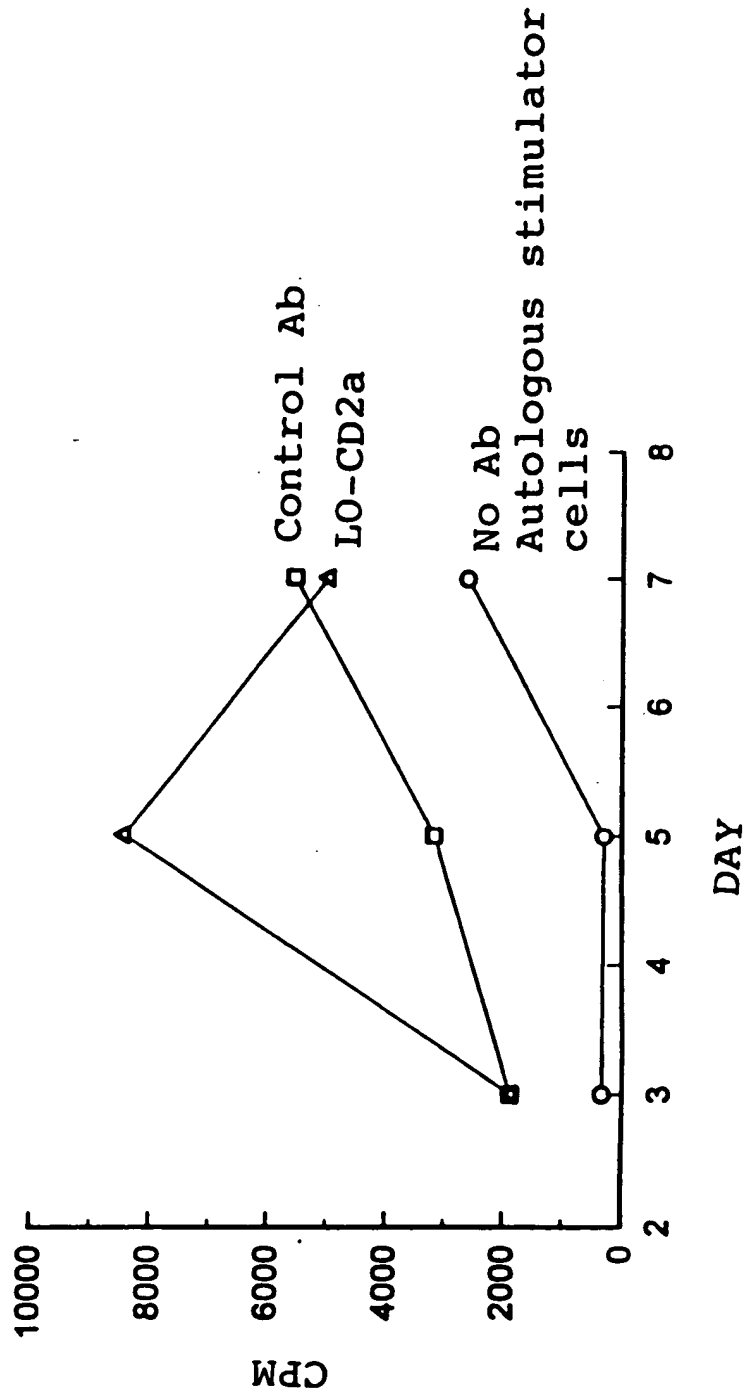


FIG. 38B



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FIG. 39

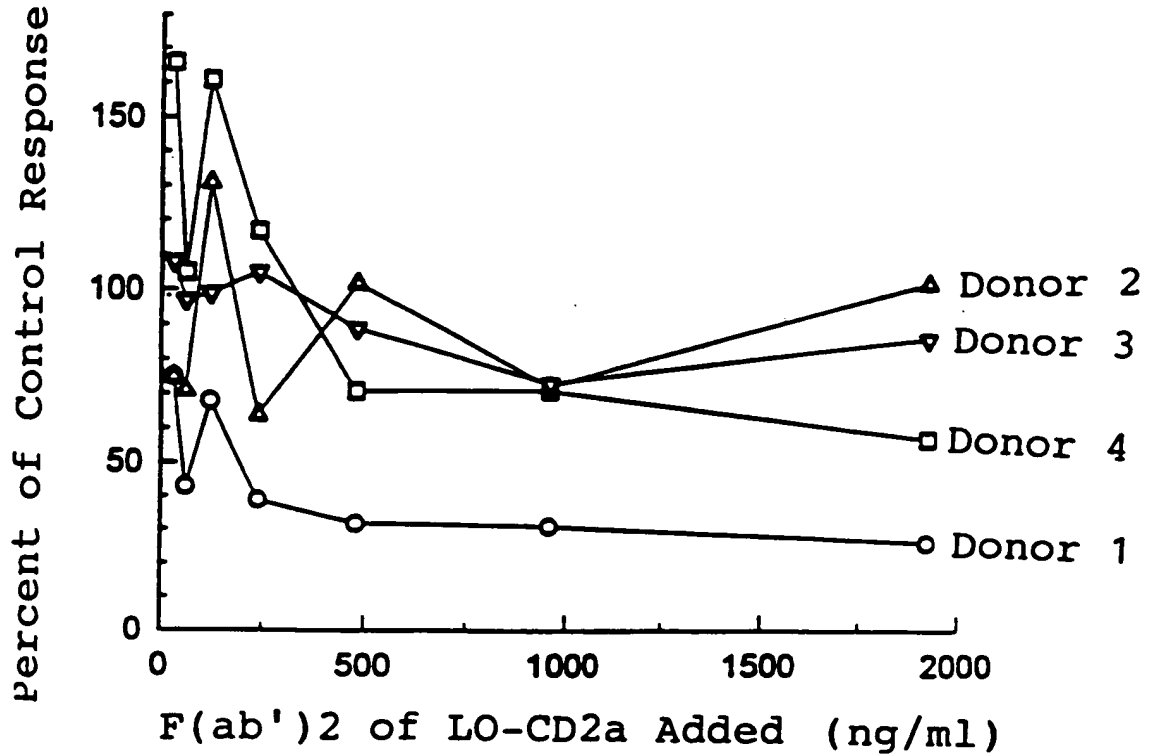


FIG. 40

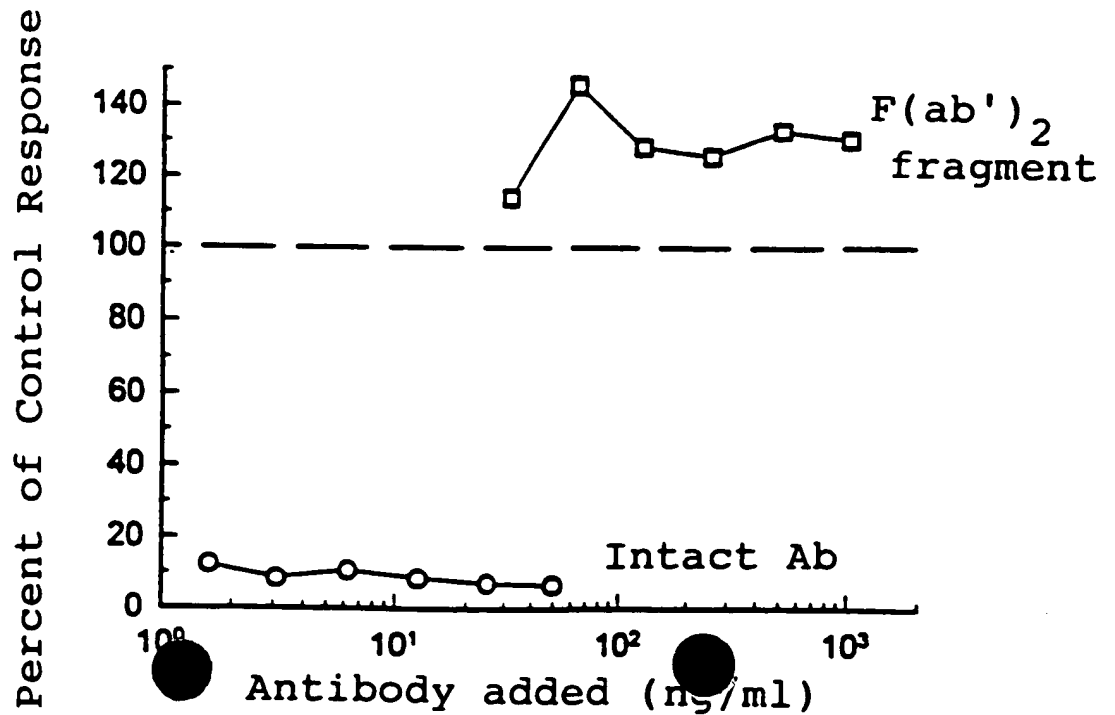


FIG. 41

